

Query Match 100.0%; Score 1610; DB 6; Length 1610;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 ATGCTCAGCTGTGGTCCCTCGCCCTGAGAGCTCTCTGTCTCAGCCGAGACTGGTTCT 120
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DB 901 AACATTTCTCATCCACCTGCTGCTGGAAGAACTCTGTAAGATGTGTTTCACTCTT 960
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QY 1021 CAAGAGTCCCGCATAGCTCTGTGCTCCAAAGAAAAGAGAGAGATCTCGAAGATCAC 1080
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RESULT 2

HUMOIPIODA 1610 bp mRNA PRI 03-AUG-1995
 LOCUS HUMOIPIODA 1610 bp mRNA PRI 03-AUG-1995
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 ACCESSION L29301
 VERSION L29301.1 GI:459831
 KEYWORDS oploid receptor.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens.

REFERENCE 1 (bases 1 to 1610)
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 Westek,A., Hurley,J.H., Bye,L.S., Campbell,A.D., Chen,X., Tian,M.,
 Liu,J., Schulman,H. and Yu,L.
 The human mu oploid receptor: modulation of functional
 desensitization by calcium/calmodulin-dependent protein kinase and
 protein kinase C

J. Neurosci. 15 (3), 2396-2406 (1995)
 JOURNAL MEDLINE
 FEATURES
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ORIGIN

Query Match 97.18; Score 1562.6; DB 6; Length 2162;

Best Local Similarity 99.78; Pred. No. 0;

Matches 1576; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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 DB 61 CGCT 120
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DB 961 TTACCGTGTCTATGAGACTGATGATCTTGGCGCTCAAGAGTGTCCGATGCTCTGTGGCT 1020
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RESULT 4
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 LOCUS HUMMORIX 2162 bp mRNA PRI 08-AUG-1994
 DEFINITION Human Mu opiate receptor (MOR1) mRNA, complete cds.
 ACCESSION L25119.1 GI:452072
 VERSION 1.1
 KEYWORDS Mu opiate receptor.
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 2162)
 AUTHORS Wang,J.B., Johnson,P.S., Persico,A.M., Hawkins,A.L., Griffin,C.A.
 and Uhl,G.R.
 TITLE Human mu opiate receptor. cDNA and genomic clones, pharmacologic
 characterization and chromosomal assignment
 JOURNAL FEBS Lett. 338 (2), 217-222 (1994)
 MEDLINE 94139928
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FEATURES	source
JOURNAL MEDLINE	Human mu opiate receptor. cDNA and genomic clones, pharmacologic characterization and chromosomal assignment
REFERENCE	FEBS Lett. 338 (2), 217-222 (1994)
AUTHORS	94139928
JOURNAL	3 (bases 1 to 1473)
	Bare, L.A.
	Direct Submission
	Submitted (24-JUL-1994) lance A. Bare, Ohmeda, FPD, 100 Mountain Avenue, Murray Hill, NJ 07974, USA
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O	y	164	TGAGCGCTTGGAAACCCGAAAGCTGTGGTGCCTCTGGCTACTCTGCACAGC - GTGCGCG	222
D	b	121	TGAGCGCTTGGAAACCCGAAAGCTGTGGTGCCTCTGGCTACTCTGCACAGCGGTGCCG	180
O	y	223	CCCGGCGCTAGTACCATGAGCAGCAGCGCTGCCCCACGAACGCCAGCATTTGCATCTGA	282
D	b	181	CCCGGCGCTAGTACCATGAGCAGCAGCGCTGCCCCACGAACGCCAGCATTTGCATCTGA	240
O	y	283	TGCGCTGGCCGACTACAGTTGGTCCCGAGACCCGACCCCGGTTCTGGTCTCACTTCTC	342
D	b	241	TGCGCTGGCCGACTACAGTTGGTCCCGAGACCCGACCCCGGTTCTGGTCTCACTTCTC	300
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D	b	301	CCACTTAGATGGCGAACCTGTGCCAGCCATGCGGTTCCGAACCGCAGCAGCTGGCGGGAG	360
O	y	403	AGACAGCCTGTGCCCTCCGACCGGCAGTCCCTCATGATCAGCGGCATCAGCATATATGC	462
D	b	361	AGACAGCCTGTGCCCTCCGACCGGCAGTCCCTCATGATCAGCGGCATCAGCATATATGC	420
O	y	463	CCTCTACCCCATCGTGTGCGGTGGGGGCTCTTCCGAACCTCTCGATCATGTATGTAT	522
D	b	421	CCTCTACTCCATCGTGTGCGGTGGGGGCTCTTCCGAACCTCTCGATCATGTATGTAT	480
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D	b	661	CAGCATATTCACCCCTGCGACCAATGATGTGATGTGATACATTTGAGTGTGCACCCGT	720
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D	b	721	CAAGGCTTATGATTTCCGTACTCCCGGAAATGCGAAATATTAATCATGTCTGCAACTGGAT	780
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D	b	781	CCCTCTTTACAGCAATTTGGTCTTCTCTGTATGTTCATGTGCTAACACAAATATACAGCAGG	840
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D	b	841	TTTCATAGATTTGACATTAATCTTCATCTCCACACTGTGTACTGGGAAACCTCTGAA	900
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QY	1362	ACCCTTCACAGGCGCAATACAGTGATGAGTAACATATCATAGTATACAAAATCTGGAAACG	1421
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QY	1422	AAAGCTCCGCTGGCCCTAACAGGGCTCTCATCCATTCGACCTTCACCAAGCTTAGAAG	1481
DB	1263	AAAGCTCCGCTGGCCCTAACAGGGCTCTCATCCATTCGACCTTCACCAAGCTTAGAAG	1322
QY	1482	CCACATCATATGTGGAGACAGGTGCTCTTCAGAAATGTGTAGAGAGCTCTAATCTCTAG	1541
DB	1323	CCACATCATATGTGGAGAGAGGTCTCTTCAGAAATGTGTAGAGAGCTCTAATCTCTAG	1382
QY	1542	AAAGTGCCTGCTTTTAG	1558
DB	1383	AAAGTGCCTGCTTTTAG	1399
RESULT	7		
PIGMOOPR	PIGMOOPR	1881 bp	mRNA
LOCUS			
DEFINITION	Sus scrofa mu opiod receptor mRNA, complete cds.		MAM 03-MAR-1999
ACCESSION	L38645		
VERSION	L38645.1		
KEYWORDS	GI:2072391		
SOURCE			
ORGANISM	Sus scrofa		
REFERENCE	Eulari-Volta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.		
AUTHORS	1 (bases 1 to 1881)		
TITLE	Pampuch M.S., Osinski M.A., Brown D.R. and Murtough M.P.		
JOURNAL	The porcine mu opiod receptor: molecular cloning and mRNA		
MEDLINE	distribution in lymphoid tissues		
REFERENCE	J. Neuroimmunol. 90 (2), 192-198 (1998)		
AUTHORS	2 (bases 1 to 1881)		
TITLE	Osinski M.A.		
JOURNAL	Direct Submission		
COMMENT	Submitted (19-SEP-1996) Mark A. Osinski, Veterinary Pathobiology,		
FEATURES	University of Minnesota, St. Paul, MN 55108, USA		
source	On May 6, 1997 this sequence version replaced gi:1553056.		
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ORIGIN			462 t
Query Match	78.1%;	Score 1258;	DB 4; Length 1881;
Best Local Similarity	88.4%;	Pred. No. 0;	
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DB	1	ATGAGCTGTGGTCTCTTAAGATGGAGAGGGGGCAACAGACAGAGATATGTCTAGAG	60
QY	64	CTCAGCTCGTCCCTCCGCGCTGACGCTCTCTGTCTGCTCAGCCAGGACTGGTTCTGTA	123

[illegible]

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Db 1378 ACACAGGATAGTAACATATCATGCTAGTAAGAAATCTGAAGCAGAAAGCTGCTGCTGC 1437
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Qy 1496 GAACAGAGGTTGCTTACAGAAATGTAGAGAGCTGCTATTTCTAGAAAGCTGCTGCTT 1555
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Db 1498 GAACAGAGGTTGCTTACAGAAATGTAGAGAGCTGCTATTTCTAGAAAGCTGCTGCTT 1557
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RESULT 8
LOCUS AF286024 1203 bp mRNA PRI 03-AUG-2000
-DEFINITION Macaca mulatta mu opioid receptor mRNA, complete cds.
ACCESSION AF286024
VERSION AF286024.1 GI:9664878
KEYWORDS
SOURCE Thesus monkey.
ORGANISM Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopitheciinae; Macaca.
REFERENCE 1 (bases 1 to 1203)
AUTHORS Miller, G.M. and Madras, B.K.
JOURNAL Cloning of the Macaca mulatta mu opioid receptor
TITLE Unpublished
REFERENCE 2 (bases 1 to 1203)
AUTHORS Miller, G.M. and Madras, B.K.
JOURNAL Direct Submission
TITLE Submitted (11-JUL-2000) Neurochemistry, New England Regional
JOURNAL Primate Research Center, Harvard Medical School, One Pine Hill
Drive, Southborough, MA 01772, USA

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CTLTSPHSMYENELKICVFIFAFIMPLVITVCGLMLIRKSRMLSGSKEXRD
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FAETAPLP"

BASE COUNT 299 a 350 c 242 g 312 t
ORIGIN

Query Match 72.5%; Score 1167.8; DB 9; Length 1203;
Best Local Similarity 98.2%; Pred. No. 4,1e-299;
Matches 1181; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
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Qy 359 CTGTCGACCCATGCGGGTCCGAACCGCAGCCTGGGCGGAGAGACAGCCTGTGCGCT 418
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 LOCUS ARI06013 1618 bp DNA PAT 14-FEB-2001
 DEFINITION Sequence 1 from patent US 6103492.
 ACCESSION ARI06013
 VERSION ARI06013.1 GI:12820078
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1618)
 AUTHORS Yu, L.
 TITLE Polynucleotide encoding mu opioid receptor
 JOURNAL Patent: US 6103492-A 115-AUG-2000.
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BASE COUNT 390 a 486 c 370 g 372 t
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 QY 686 TACTATACATGTTTACACAGATATTCACCTCTGACCATGAGTGTGATGATACATT 745
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JOURNAL J Biol. Chem. 270 (26), 15877-15883 (1995)
MEDLINE 95318184
REFERENCE 2 (bases 1 to 2229)
AUTHORS Evans, C.C.
TITLE Direct Submission
JOURNAL Submitted (04-JAN-1995) Christopher J Evans, Psychiatry and
Biobehavioral Sciences, University of California at Los Angeles,
UCLA-NPI, 760 Westwood Plaza, Los Angeles, CA 90024-1759, USA

FEATURES
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BASE COUNT 562 a 608 c 489 g 570 t
ORIGIN

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Best Local Similarity 83.4%; Pred. No. 6, 2e-287;
Matches 1324; Conservative 0; Mismatches 255; Indels 9; Gaps 4;

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• Thu May 2 11:42:20 2002

us-08-305-518-7.rge

Page 17

Search completed: May 1, 2002, 22:13:58
Job time: 8060 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 1, 2002, 21:07:23 ; Search time 181.1 Seconds
(without alignments)
7621.721 Million cell updates/sec

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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 930621 seqs, 428662619 residues
Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1610	100.0	1610	21	AAAS9503 cDNA encoding a hu
3	1562.6	97.1	2162	19	AAV61984 Human mu-oploid re
4	1562.6	97.1	2162	19	AAV61995 Human mu-oploid re
5	1561	97.0	2162	19	AAV61985 Human mu-oploid re
6	1561	97.0	2162	19	AAV61986 Human mu-oploid re
7	1561	97.0	2162	19	AAV61987 Human mu-oploid re
8	1561	97.0	2162	19	AAV61988 Human mu-oploid re
9	1561	97.0	2162	19	AAV61989 Human mu-oploid re
10	1561	97.0	2162	19	AAV61990 Human mu-oploid re
11	1561	97.0	2162	19	AAV61991 Human mu-oploid re

12	1561	97.0	2162	19	AAV61992 Human mu-oploid re
13	1561	97.0	2162	19	AAV61993 Human mu-oploid re
14	1561	97.0	2162	19	AAV61994 Human mu-oploid re
15	1553	96.5	2160	16	AAO93102 Human mu opiate re
16	1553	96.5	2162	21	AAZ88470 Human mu oploid re
17	1123.8	69.8	1618	16	AAO89222 Rat mu oploid rece
18	1123.8	69.8	1618	16	AAO89223 Transcription regu
19	1123.8	69.8	1618	21	AAAS9499 cDNA encoding a mu
20	1122.6	69.7	2229	19	AAV49252 Mouse mu opiate re
21	1114.6	69.2	1981	22	AAD11041 Murine delta opioi
22	1113	69.1	1981	15	AAO56705 Partial sequence o
23	1110.4	69.0	1610	21	AAZ60741 cDNA encoding mur1
24	1031.6	64.1	2135	22	AAZ60726 Nucleotide sequenc
25	971.2	60.3	2070	15	AAO79199 Rat mu-subtype opi
26	926.8	57.6	1542	21	AAZ60729 cDNA encoding mur1
27	925.4	57.5	1365	21	AAZ60737 cDNA encoding mur1
28	925.4	57.5	1365	21	AAZ60736 cDNA encoding mur1
29	925.4	57.5	1423	21	AAZ60726 cDNA encoding mur1
30	924	57.4	1334	21	AAZ60734 cDNA encoding mur1
31	924	57.4	1729	21	AAZ60734 cDNA encoding mur1
32	922.4	57.3	2045	21	AAZ60735 cDNA encoding mur1
33	808.2	50.2	1238	21	AAZ60727 cDNA encoding mur1
34	713	44.3	1257	21	AAZ60730 cDNA encoding mur1
35	698.4	43.4	830	22	AAD11039 Human mu oploid re
36	694.2	43.1	829	15	AAO56703 Human kappa oploid
37	457.4	28.4	1275	18	AAZ92601 Sequence of murine
38	443.2	27.5	1821	15	AAO56700 Murine delta opioi
39	443.2	27.5	1829	22	AAD11035 Mouse delta opiate
40	443.2	27.5	2218	19	AAV49253 Mouse delta opiate
41	443.2	27.5	2272	16	AAO75927 DNA encoding a mu3
42	441	27.4	441	20	AAZ59781 Human kappa oploid
43	434.8	27.0	1142	17	AAZ12550 Human kappa oploid
44	434.8	27.0	1143	18	AAZ90998 Human kappa oploid
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ALIGNMENTS

RESULT 1	AAO89226	standard: cDNA, 1610 BP.
ID	AAO89226	
XX	AAO89226:	
AC	20-OCT-1995	(first entry)
XX		
DT		
XX		
DE		Human mu oploid receptor cDNA.
XX		
KW		Mu oploid receptor; MOR; gene therapy; diagnostic; ss.
OS		Homo sapiens.
XX		
FT	Key	Location/Qualifiers
FT	CDS	239..1441
FT		/*tag= a
XX		
PN	W09507983-A.	
XX		
PD	23-MAR-1995.	
XX		
PF	13-SEP-1994;	94WO-US10358.
XX		
PR	13-SEP-1993;	93US-0120601.
XX		
PA	(INDV) UNIV INDIANA FOUNO.	
XX		
PI	Yu L;	
XX		
DR	WPI: 1995-131351/17.	
XX	P-PSDB: AAR71966.	
XX		
PT	New nucleic acid encoding new human mu oploid receptor - and	

PT related vectors, transformed cells, antibodies etc., useful in
PT diagnosis, treatment and drug screening.

XX Claim 5: Page 208-210; 266pp: English.

XX A cDNA library constructed from human caudate nucleus mRNA was
CC screened with rat mu opiod receptor cDNA under conditions of
CC low stringency. One positive clone included the sequence given in
CC AA089226, encoding a mu opiod receptor MOR (AAR1964). The cDNA
CC is used for prodn. of recombinant MOR, in gene therapy, etc.
XX

SO Sequence 1610 BP; 384 A; 467 C; 359 G; 400 T; 0 other;

Query Match 100.0%; Score 1610; DB 16; Length 1610;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGATGACCTGTGTGAATCTAAGTGGAGGGGCTATACCGACAGAGAAATGTGAC 60
DB 1 cggatgacctgtgtgaactactaagglygaggggtatacagcagagagatgacg 60

QY 61 ATGCTAGCTGGTCCCGCTGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
DB 61 atgctagctgggtcccgctgacgctctctctctctctctctctctctctctct 120

QY 121 GTAAGAAACAGCAGAGCTGTGGCAGGCGAAAGAGCGGCTGAGCGCTTGAACCC 180
DB 121 gtaagaaacagcagagctgtggcagggcgaaagagcggtgagcgcttgaaccc 180

QY 181 GAAAGCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 181 gaaagctctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 240

QY 241 GGACAGAGCGGTCGCCCGCAGAACGCCACAAATGTGACATGATGCTGGCGTCAAG 300
DB 241 ggacagagcggtcgcccgagaaacgcccaaatgtgacatgctggcggtcaag 300

QY 301 TTCTCTCCCGACGACCGACGCCGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
DB 301 ttctctcccgacgacgacgccggttctgctgctgctgctgctgctgctgctgct 360

QY 361 GTCCGACCCATGCGGCTCCGAACCGACGACCTGGCGGAGAGACAGCTGTGCCCTCC 420
DB 361 gtccgacctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 420

QY 421 GACCGGAGTCCTCCATGTCAGGCGCATCAGATGATGCTGCTGCTGCTGCTGCTGCT 480
DB 421 gaccggagtcctccatgtcagcgccatcagatgctgctgctgctgctgctgctgct 480

QY 481 CGTGTGGGGCTCTTGGAAACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
DB 481 cgtgtgggctcttggaaacttctgctgctgctgctgctgctgctgctgctgctgct 540

QY 541 GAAAGCTGCGCACAACATCTACATTTTCAACCTTGGCTGCGAGATGCTTACCGACAG 600
DB 541 gaaagctgcgccacaacatctacatTTTTCAACCTTGGCTGCGAGATGCTTACCGACAG 600

QY 601 TACCCTGCGCTTCAGAGTGTGAATTAACATGGAAGAAATGGCAATTTGGAACCAATCCT 660
DB 601 taccctgcgcttccagagtgtgaatttaacatggaaagaaatggcaatTTGGAACCAATCCT 660

QY 661 TTGCAAGATAGTATCTCATATATTACTTAACATGTTACACAGCATATATCAACCTCTG 720
DB 661 ttgcaagatagtatctcatatATTACTTAACATGTTACACAGCATATATCAACCTCTG 720

QY 721 CACCATGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
DB 721 caccatgagtggtgattgattgattgattgattgattgattgattgattgattgattgatt 780

QY 781 TACTCCCGGAATGCAAAATTAATCAATGTCGAATGATGATGATGATGATGATGATGAT 840
DB 781 tactcccggaatgcaaaatTAATCAATGTCGAATGATGATGATGATGATGATGATGAT 840

QY 841 TCTTCTGTAATGTCATGCTGCTACAAACAAATACAGCAAGGTTCCATGATGTGACACT 900
DB 841 tcttctgtaatgctcatgctgctacaaacaaatACAGCAAGGTTCCATGATGTGACACT 900

QY 901 AACATTCTCTCATCAACCTGTGACTGGGAAAACCTGCTGAAGATGTGTTTCTACTT 960
DB 901 aacatttctctcatcaacctgtgactgggaaaacctgctgaagatgtgtttctactt 960

QY 961 CGCCTTCATTATGACGATGCTCATATTAACCGGTGCTGCTGCTGCTGCTGCTGCTGCT 1020
DB 961 cgccttcatTATGACGATGCTCATATTAACCGGTGCTGCTGCTGCTGCTGCTGCTGCT 1020

QY 1021 CAAGAGTTCGCCGATCTCTGCTGCTCAAGAAAGAAAGAGCAGAGATCTTGAAGATCAC 1080
DB 1021 caagagtTCGCCGATCTCTGCTGCTCAAGAAAGAAAGAGCAGAGATCTTGAAGATCAC 1080

QY 1081 CAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
DB 1081 caggatgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 1140

QY 1141 CGTCATCATTAAGCCTTGCTGCTTACATCCAGAAACTTACGTTCCAGACTGTTCTTGGA 1200
DB 1141 cgtcacatTAAGCCTTGCTGCTTACATCCAGAAACTTACGTTCCAGACTGTTCTTGGA 1200

QY 1201 CTTCGATTTGCTCTAGGTTACAAACAGCTGCTCAACCCAGTCTTTATGCAATTTCT 1260
DB 1201 cttcgattTGCTCTAGGTTACAAACAGCTGCTCAACCCAGTCTTTATGCAATTTCT 1260

QY 1261 GGATGAAACTTCAACGATGCTTTCAGAGAGTCTTATGCCAAGCTTTCACACTTTTA 1320
DB 1261 ggatgaaacttcaacgattTTCAGAGAGTCTTATGCCAAGCTTTCACACTTTTA 1320

QY 1321 GCACAAAACCTCCACTGCAATTCGTCAGAACACTAGACCAACCCCTCCAGCGCAATAC 1380
DB 1321 gcacaaaactccactgcaattTCGTCAGAACACTAGACCAACCCCTCCAGCGCAATAC 1380

QY 1381 AGTGATAGAACTATCATCAGCTAGAAAATCTGGAAGCAGAAATGCTCGGTTGCCCTA 1440
DB 1381 agtgatAGAACTATCATCAGCTAGAAAATCTGGAAGCAGAAATGCTCGGTTGCCCTA 1440

QY 1441 ACAGGTCCTCATGCTTCCGACCTTCACCAAGCTTGAAGCCACATATATGTGGAAC 1500
DB 1441 acaggctcctcatgcttccgacctTCACCAAGCTTGAAGCCACATATATGTGGAAC 1500

QY 1501 AGGTGCTTCAAGATGTGAGAGGCTTAATCTCTAGAAAGGCTGCTTTAGGT 1560
DB 1501 aggtgcttCAAGATGTGAGAGGCTTAATCTCTAGAAAGGCTGCTTTAGGT 1560

QY 1561 CATCAACCTTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1610
DB 1561 catcaacctTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1610

RESULT 2

AAA59503
ID AAA59503 standard; cDNA: 1610 BP.

XX AC AAA59503;

XX AC 14-NOV-2000 (first entry)

XX DE cDNA encoding a human mu opiod receptor polypeptide.

XX DE mu opiod receptor; transcription regulatory polypeptide;

XX DE opiod receptor-like polypeptide; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT CDS 239..1441
FT /tag= a "mu opiod receptor"

XX US6103492-A.
PN
XX
PD 15-AUG-2000.
XX
PF 07-JUL-1997; 97US-0889108.
XX
PR 13-SEP-1994; 94US-0305518.
PR 08-MAR-1993; 93US-0056886.
PR 13-SEP-1993; 93US-0120601.
XX
PA (INDY) UNITV INDIANA.
PI Yu L;
DR WPI: 2000-542550/49.
DR P-PSDB; AAB07866.
XX
PT Novel nucleic acids encoding mu opiod receptor for expressing large
PT quantities opiod receptors which are useful for screening and
PT evaluating subtype-selective drugs and as probes or primers -
XX
PS Claim 17; Column 99-102; 86pp; English.
XX
XX The present sequence encodes a mu opiod receptor protein. The
CC specification also describes a transcription regulatory polypeptide
CC and an opiod receptor-like polypeptide. Human mu opiod receptor
CC polynucleotides are useful as a source of probes and primers, which
CC may be used as diagnostic tools to detect normal and abnormal DNA
CC sequences in DNA derived from patients cells. They are also used as
CC a means for detecting and isolating other members of the polypeptide
CC family and related polypeptides from a DNA library potentially
CC containing such sequences. The polynucleotide is used for preparing
CC large quantities of opiod receptor which on expression in
CC microorganism can be useful for evaluating subtype-selective drugs.
XX
SQ Sequence 1610 BP; 384 A; 467 C; 359 G; 400 T; 0 other;

Query Match 100.0%; Score 1610; DB 21; Length 1610;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGATGAGCCTGTGTAACCTAAGTGGAGGGGCTATACGACAGAGAATGTCA 60
DB 1 cggatgagcctgtgtaacctaagtggaggggctatacgacagagaatgtcag 60
QY 61 ATGCTAGCTCGGTCCCTCCGCTGAGCGTCTCTGTGCTAGCCAGACTGTTTCT 120
DB 61 atgctagctcgggtccctccgctgagcgtctctgtgctagccagactgtttct 120
QY 121 GTAAAGAAAGACGAGAGCTGTGGCAGCGGGAAGAGCGCTGAGGGCTTGAACCC 180
DB 121 gtaagaaagacgagagctgtggcagcgggaaagagcgctgagggcttgaaccc 180
QY 181 GAAAGTCTCGTGTCTGCTACTCGACAGCTGCCGCCGCCGCTGAGTACCAT 240
DB 181 gaaagtctcgtgtctgctactcgcacagctgccgccgccgctgagtcacat 240
QY 241 GGACAGACGCGTGCCTGCCCAAGACGCAATTCAGTACTGATGCTTGCGCTAC 300
DB 241 ggacagacgctgctgcctgcccaagacgcaattcagtactgatgcttgcgctac 300
QY 301 TTGCTCCCGACGACCGCCGCTGCTGGGTCACCTTGCCACTTGGATGGCAACCT 360
DB 301 ttgctcccgacgacccgctgctgggtcaccttgccacttggatggcaacct 360
QY 361 GTCCGACCATGCGGTCCGAACCGACGACCTGGCGGAGAGACAGCCTGTCCTCC 420
DB 361 gtccgaccatgcggtccgaaccgacgacctggcggagagacagcctgtcctcc 420
QY 421 GACGGCAGTCCCTCATGTATCAGGCGCATCAGATCATAGGCCCTTACTCCATG 480
DB 421 gacggcagtcctcatgtatcaggcgcatcagatcataggcccttactccatg 480

DB 421 gaccggcaagtcctccatcagatcagcgcatcagatcagtcagtccttactccatc 480
QY 481 CGTGGTGGGGCTTTGGAAACTTCTGGTCAATGATGATGATGATGATGATGATGAT 540
DB 481 cgtgggtgggctttggaaacttctgggtcaatgatgatgatgatgatgatgatgat 540
QY 541 GAAGACTGGCCACCAACATCTACATTTTCAACCTGCTGCGAGATGCTTGAACCA 600
DB 541 gaagactggccaccacacatctacatlttcaacctgtctgagagatgcttgaaccag 600
QY 601 TACCTGCTCCCTTCAGAGTGTGAATTAATGGCAACATGGCCATTGGAAACCAT 660
DB 601 tacctgctcccttcagagtgtgaattaatggcaacatggccatttggaaaccat 660
QY 661 TTGCAAGATAGTATCTCATGATATTAACATGTTTACACAGCATATTAACCTCTG 720
DB 661 ttgcaagatagtatctcatgatattaacatgttttacacagcatatataacctctg 720
QY 721 CACCATGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 780
DB 721 caccatgagtgatgatatgatatgatatgatatgatatgatatgatatgatatg 780
QY 781 TACTCCCGCAATGCAAAATTAATCAATGTCTGCAACTGGATCTCTTCAGCCATT 840
DB 781 tactcccgcaatgcaaaatatacaatgtctgcaactggatctcttcagccattg 840
QY 841 TCTTCTGTAATGTTATGATGATGATGATGATGATGATGATGATGATGATGAT 900
DB 841 tcttctgtaatgttatgattgattgattgattgattgattgattgattgattgatt 900
QY 901 AACATTCTCTCATCAACCTGTACTGAGGAAAACCTGTGAAGATCTGTGTTTCA 960
DB 901 aacattctctcatcaacctgtactgaggaaaacctgtgaagatctgtgtttca 960
QY 961 CGCTTCATTAATGCAAGTGTCTATCAATTCAGTGTCTTGTGATGATGATGAT 1020
DB 961 cgcttcattaatgcaagtgtctatcaatttcagtgtcttgtgatgatgatgat 1020
QY 1021 CAAGAGTGTCCGATGCTCTGCTGCTCCAAAGAAAAGACAGCAATCTTGAAGAT 1080
DB 1021 caagagtgtccgatgctctgctgctccaaagaaaagacagcaatcttgaagat 1080
QY 1081 CAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
DB 1081 cagagtgtgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 1140
QY 1141 CGTCATCATTTAAAGCTTGGTTACAAATCCCAAGAAATACGTTCCAGACTGTT 1200
DB 1141 cgtcatacatttaagcttggttacaaatcccaagaaatacgttccagactgtt 1200
QY 1201 CTTTCTGATTTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1260
DB 1201 ctttctgatTTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1260
QY 1261 GGATGAAAATCTTCAAAAGATGCTTCAAGAGATGTTCTGATGCCAACCTCTT 1320
DB 1261 ggatgaaaatctttaaaagatgcttcaagagatgttctgatgccaacctctt 1320
QY 1321 GCAACAAAATCTGACATGCAATTCGTAGAACACTAGAGACACCCCTCCAGG 1380
DB 1321 gcaacaaaatctgacatgcaattcgtagaaactagagacacccctccagg 1380
QY 1381 AGTGATAGACATTAATCATCAGCTAGAAAATGTGGAAGAGAAAGCTGCTG 1440
DB 1381 agtgatagacatTAATCATCAGCTAGAAAATGTGGAAGAGAAAGCTGCTG 1440
QY 1441 ACAGGCTTCATGCCATTCGACCTTACCAAGCTTGAAGGCCACCATGATGAT 1500
DB 1441 acaggcttcataGCCATTCGACCTTACCAAGCTTGAAGGCCACCATGATGAT 1500
QY 1501 AGTTGCTTCAGAAATGTTAGAGAGCTTAATTTCTAGGAAAGTGCCTGCTT 1560
DB 1501 agttgcttcagaaatgTTAGAGAGCTTAATTTCTAGGAAAGTGCCTGCTT 1560

OY	1561	CATCCACCTCTTTCTCCTCTGTGGCCACTGCTGTGCATTAGAGCGC	1610
Dd	1561	caccacaccttcctcctcgtgcccactctgcctctgacattagagccg	1610
RESULT	3		
ID	AAV61984	standard; cDNA; 2162 BP.	
XX	AAV61984		
AC	AAV61984;		
XX			
DT	11-JAN-1999	(first entry)	
XX			
DE	Human mu-opioid receptor cDNA.		
XX			
KM	Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;		
KM	preposition; addiction; analgesic; anaesthetic; anti-addictive;		
KW	psychopharmaceutical agent; diagnostic; side effect; drug; opiate;		
KM	cocaine; inherited alcoholism; human; ss.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	location/Qualifiers	
FT	CDS	213..2040	
FT		/tag= a	
FT		/product= "mu-opioid receptor"	
FT	misc_feature	502..503	
FT		/tag= b	
FT		/note= "Site of intron 1"	
FT	misc_feature	855..856	
FT		/tag= C	
FT		/note= "Site of intron 2"	
FT	misc_feature	1376..1377	
FT		/tag= d	
FT		/note= "Site of intron 3"	
XX			
PN	WO9839397-A2.		
XX			
PD	06-AUG-1998.		
XX			
PF	02-FEB-1998;	98WO-DE00382.	
XX			
PR	03-FEB-1997;	97DE-I003925.	
XX			
PA	(DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.		
XX			
PI	Hoehe M., Wendel B;		
XX			
DR	WPI; 1998-437487/37.		
XX			
PT	New genomic and cdna sequences encoding human mu-opioid receptor -		
PT	used, e.g. to predict pre-disposition to addiction and for		
PT	development of analgesics, anaesthetics and anti-addiction agents		
PS			
XX	Claim 8; Page 14-15; 26pp; German.		
XX			
CC	This sequence encodes a novel human mu-opioid receptor. This sequence and		
CC	its variants, polymorphisms and mutants are used in a method for		
CC	detecting predisposition to disease, particularly addictive disease, by		
CC	isolating DNA from a sample, genotyping selected positions and comparing		
CC	with a reference DNA. Such sequences are used to develop analgesic,		
CC	anaesthetic, anti-addictive and psychopharmaceutical agents, to construct		
CC	genes and vectors, particularly for pharmaceutical development, to		
CC	develop diagnostic kits for predicting risk of addiction, response to		
CC	analgesics or anaesthetics, or development of side effects from a drug.		
CC	Particular applications are to determine risk of addiction to opiates or		
CC	cocaine, or of developing inherited alcoholism.		
XX			
SQ	Sequence 2162 BP; 562 A; 565 C; 458 G; 575 T; 2 other;		

	Best Local Similarity	99.7%	Pred. No. 0:	Matches 1576:	Conservative	0:	Mismatches	4:	Indels	1:	Gaps	1:
QY	28	TGGGAGGGGGCTATACGAGAGAGAAATGTCAAGTGTCTACGTCGGTCCCTCCGCTGA	87									
Db	1	tggagagggggtatacagcagagagaaatgtcagatgtctcagctgcgtccctccgcttga	60									
QY	88	CGCTCTCTCTGTCTTCACAGCAGAGACTGGTTCTGTAAAGAACAGAGAGAGCTGTGGACG	147									
Db	61	cgtccctctctgtctccagccagagacttgttctgtaaagaacaagaagagctgtgtgcgc	120									
QY	148	GGCGAAAGGAAGCGGCTATAGCGGCTTGGCAACCCGAAAAGTCTCGGTGCTCTGTGACT	207									
Db	121	ggcgaaaggaagcvgctgaagcgcttggaaacccgaaaagtctcgtgtctctgttacct	180									
QY	208	CGCACAGC-GTGCCTCGCCCGCGCTGACGTACCATGAGACAGACGCGCTGCCACGAACG	266									
Db	181	cgcacagcgtgtccgcgcgcgtcagtlacatlgacagcagcgtgcgcccaagcagc	240									
QY	267	CGAGCAATTGGACCTGATGCTGGGGGTACTCAAGTTGCTCCCGACACACCGCCGGATT	326									
Db	241	ccagcaaatgtccctgtatgtcttgggtactcgaatgttctcccacacccagccccgtt	300									
QY	327	CTGTGGTCAACTTGTCCCACTTAGATGAGCAACCTGTCCGACCATGCGGTCCGAACCGCA	386									
Db	301	ctgtgttcaactgtgtcccaacttagatgtgcaacctgtccgacctatgtgtccgaacgca	360									
QY	387	CGGACCTGGGGGGGAGAGACACACCTGTGCTCCGACCGGCAAGTCCCTTCATGATCACGG	446									
Db	361	ccaacctggcgggagagacagcctgtgtccctccgacccgagctccctccatgatcacgg	420									
QY	447	CCATCAGCATCATGTGCGCTTACTCTCATCGTGTGGTGGGGGCTCTTGGAAACTTCC	506									
Db	421	ccatcagcatcatgtgcctcttacctcatcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	480									
QY	507	TGGTATGTATGTGATTTGTGCAGATACACAGAGATAAAGCTGCCACCAACATCTTCAATT	566									
Db	481	tgttatgtatgtatgtgtgtcagatatcaccaagaatgaagactgtcccaacaacttcaatc	540									
QY	567	TCAACCTTGCTGTGCAGATGCTTACAGGCACACAGTACCTGCTTCCAGATGTGAATT	626									
Db	541	tcaacctgtgtctgtgcagatgtccttagcacaacagtaacctgtcccttccagatgtgaatt	600									
QY	627	ACCTAATGGGAACATGSCCATTTGGAACATCCTTTCGAAGATAGTATCTCCATAGATT	686									
Db	601	acctaatggaacaatgtgcattgtgaacatccttcttgaagaatgaatgtcttccatagatt	660									
QY	687	ACTATAATGTATTCACGACGATTTCAACCTGTGCACATGAGTGTTCATGATTCATTTG	746									
Db	661	actataaacaatgttccacagcatatccacccttgcacaagaatgtgtatcgtatcatgt	720									
QY	747	CAGTGTGCACCCCTGTCAAGGCTTAGATTTCGTACTCCCGAAATGCCAAATTTATCA	806									
Db	721	cagttgtcacaccctgttcaagccttagattttccgtactcccgaaatgtccaaatatca	780									
QY	807	ATGTGTGAACGTGATCCCTCTTAGGCATTTGGCTTCTGTATGTTCATGGTACTAA	866									
Db	781	atgttctgaacatgtgtcccttccacgcatgtgttcttcgtaaatgttcatatgtctacaa	840									
QY	867	CAAAATACAGCGAAGTTCCATAGATTGTACACTAACATTTCTTCATCCAACTGTACT	926									
Db	841	caaaatacaggaagtctccatagattgtlactactaaacttctcatccaaacctgtact	900									
QY	927	GGGAAACCTGCTGAAGATCTGTCTTTTCATCTTCGCTTCAATTATGCAAGTGCATCA	986									
Db	901	gggaaacctcgttgaagatctgtgttttcatcttctgcctcaattatgtccagtgctcatca	960									

Db 1021 ccaaaagaaagcagcgaactcttcgaagatcacccagatggtgctggtggtggtgctg 1080
QY 1107 TGTTCATGCTGCTGGAGACTCCCATTCACATTTAGCTCATATTAAGCGCTTGTTACAA 1166
Db 1081 tgtcatcgtctcgtcgtgactcccatcattacgtatcattcaatgaagccttggttaca 1140
QY 1167 TCCGAGAACTACGTTCCAGACTGTTTCTTGCGACTTTCGACTTGTCTAGGTTACACA 1226
Db 1141 tcccgaactcagctcagactgttcttgacacttcgtcattgctcctaggttacacaa 1200
QY 1227 ACAGCGCTCAACCCAGTCCCTTATGATTTCTGGATGAAGCTTCAACAGATGCTTCA 1286
Db 1201 acagctgcctcaaccagctcccttaccatctcgtatgataaactcaacgaagcttca 1260
QY 1287 GAGAGTTCTGTATCCCAACCTCTTCCACATTTAGCAACAAACTCCACTCGAATTCGTC 1346
Db 1261 gagagctcgtatcccaactcttcaaatgtgagcaaaaaccccaactcgaattcgtc 1320
QY 1347 ACAACACTAGAGACCAACCCCTTCACGCGCCATACAGTGATGAACTAATCATCAGCTAG 1406
Db 1321 agaacactagagaccacccctcacgccaatacagtgatagaactaatacactagctag 1380
QY 1407 AAAATCTGGAACGAGAACTGCTCGGTCCTTAACAGGCTCATGTCATTCGACCTT 1466
Db 1381 aaaaactgaaagcagaactcgtccgttgccttaacaggtctatcgtccatccgaactt 1440
QY 1467 CACCAAGCTTAGAACCAACATGATGTGGAAGCAGGTTGCTTCAAGATGTGTAGAGAG 1526
Db 1441 caccgaagcttagaagcaccatcgtatgtgaaagcaggtgtcctcaagaatgtgtaggaag 1500
QY 1527 CTCTAATCTCTAGAGAACTGCTGCTTTTAGGTATCCACCTCTTCTCTGAGCCA 1586
Db 1501 cctcaattctcaggaagaagtgctactttagtgatcccaactcttctcctcgtgcca 1560
QY 1587 CTCTGCTGCACATTTAGAGG 1607
Db 1561 cctcgtctcgcacatcagaag 1581

RESULT 4
AAV61995
ID AAV61995 standard; cDNA: 2162 BP.
XX
AC AAV61995;
DT 11-JAN-1999 (first entry)
XX
DE Human mu-opioid receptor cDNA variant 11.
XX
KW Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
KW prediisposition; addiction; analgesic; anaesthetic; anti-addictive;
KW psychopharmacological agent; diagnostic; side effect; drug; opiate;
KW cocaine; inherited alcoholism; human; ss.
XX
OS Homo sapiens.
OS Synthetic.
OS
FH Key Location/Qualifiers
FT CDS 213..2040
FT FT /*tag= a
FT FT /*product= "mu-opioid receptor"
FT FT /*tag= b
FT FT /*tag= "Site of intron 1"
FT FT /*note= 855..856
FT FT misc_feature
FT FT /*tag= C
FT FT /*note= "Site of intron 2"
FT FT misc_feature
FT FT /*tag= d
FT FT /*note= "Site of intron 3"
FT FT mutation
FT FT 1613
FT FT /*tag= e
FT FT /*note= "Wild type G is replaced by C"

XX
PN W09833937-A2.
XX
PD 06-AUG-1998.
XX
PE 02-FEB-1998; 98WO-DE00382.
XX
PR 03-FEB-1997; 97DE-1003925.
XX
PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
PI Hoehe M, Wendel B;
XX
DR WPI: 1998-437487/37.
XX
PT New genomic and cDNA sequences encoding human mu-opioid receptor -
PT used, e.g. to predict pre-disposition to addiction and for
PT development of analgesics, anaesthetics and anti-addiction agents
XX
PS Claim 8; Page -: 26pp; German.
XX
CC This sequence encodes a novel human mu-opioid receptor in which a G
CC nucleotide at position 1613 of the wild-type sequence represented in
CC AAV61984 is replaced by a C. The wild type receptor and its variants,
CC polymorphisms and mutants are used in a method for detecting
CC prediisposition to disease, particularly addictive disease, by isolating
CC DNA from a sample, genotyping selected positions and comparing with a
CC reference DNA. Such sequences are used to develop analgesic,
CC anaesthetic, anti-addictive and psychopharmacological agents, to construct
CC genes and vectors, particularly for pharmaceutical development, to
CC develop diagnostic kits for predicting risk of addiction, response to
CC analgesics or anaesthetics, or development of side effects from a drug.
CC Particular applications are to determine risk of addiction to opiates or
CC cocaine, or of developing inherited alcoholism.
CC Note: This sequence is not represented in the specification and has
CC been constructed from the wild-type sequence represented in AAV61984 in
CC accordance with the specification.
XX
SQ Sequence 2162 BP; 562 A; 566 C; 457 G; 575 T; 2 other;

Query Match 97.1%; Score 1562.6; DB 19; Length 2162;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1576; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
QY 28 TGGAGGGGGCTATACGAGAGAGATGTGATGCTCAGCTCGCTCCGCTCGA 87
Db 1 tggaggggggctatacagcagaagaatgctcagatgctcgtccctccgcctga 60
QY 88 CGCTCCTCTGTCTTCACGACGAGACTGTTCTGTAGAAACAGCAGAGCTGTGGACG 147
Db 61 cgtctctctcgtctcagcagcagactggttcttgaagaacagcagcgtgtgcaagc 120
QY 148 GCGGAAAGGAGAGCGGCTGAGGCGCTTGGACCCGAAAAGTCTCGGTCTGCTTACT 207
Db 121 ggcgaagaagcagcgtcgtgagcgttggaaccgaaagctcgtgtgtcctgtactt 180
QY 208 CGCACAGC-GTGCAGCGCCGCGCGCTCATACATGAGAGAGCAGCGCTCCGACAGAG 266
Db 181 cgcacaagcgtgtcccgccgcgcgtcagatcattgagacagcagcgtgtccccaagacg 240
QY 267 CCAGCAATTGCATGATGCTTGGCGTACTCAAGTTGCTCCCGACACCCAGCCGGT 326
Db 241 ccagcaattgcatgtcgttgcgttactcaagttgtctcccaagcaccagcccggtt 300
QY 327 CCTGGGTCAACTTGTCCCACTAGATGGAACCTTCCGACCCATGCGGTCCGAACGCA 386
Db 301 cctgggtcaactgttcccaacttagatggaacctgtccgaaccatgtggtccgaacgca 360
QY 387 CCGACTGGGCGGAGAGACAGCCCTGTCCCTCCAGCCGAGAGTCCCTCATGATCAGG 446
Db 361 ccaacttggcggtgagagacagcctgtgctcctccagccgagctcctcatgatcaag 420

[illegible]

Db	1501	ctctaatctcttaggaagagcgtactttagtgatcatccaactcttctctcgcca	1560
Oy	1587	CTCTGCTCTGCACATAGAGG	1607
Db	1561	ctctgctctgcacattagagg	1581
RESULT 5			
AAV61985			
ID	AAV61985	standard; cDNA; 2162 BP.	
XX			
AC	AAV61985;		
XX			
DT	11-JAN-1999	(first entry)	
XX			
DE	Human mu-opioid receptor cDNA variant 1.		
XX			
KM	Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;		
KM	predisposition; addiction; analgesic; anaesthetic; anti-addictive;		
KW	psychopharmaceutical agent; diagnostic; side effect; drug; opiate;		
KM	cocaine; inherited alcoholism; human; ss.		
XX			
OS	Homo sapiens.		
OS	Synthetic.		
XX			
FH	Key	Location/Qualifiers	
FH	CDS	213..2040	
FT		/*tag- a	
FT		/product= "mu-opioid receptor"	
FT	misc_feature	502..503	
FT		/*tag- b	
FT		/note= "Site of Intron 1"	
FT	misc_feature	855..856	
FT		/*tag- c	
FT		/note= "Site of intron 2"	
FT	misc_feature	1376..1377	
FT		/*tag- d	
FT		/note= "Site of Intron 3"	
FT	mutation	41	
FT		/*tag- e	
FT		/note= "Wild type G is replaced by T"	
PN	W09833937-A2.		
XX			
PD	06-AUG-1998.		
XX			
PF	02-FEB-1998;	98WO-DE00382.	
XX			
PR	03-FEB-1997;	97DE-1003925.	
XX			
PA	(DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.		
XX			
PI	Hoehle M, Wendel B;		
XX			
DR	WPI: 1998-437487/37.		
XX			
PT	New genomic and cDNA sequences encoding human mu-opioid receptor -		
PT	used, e.g. to predict pre-disposition to addiction and for		
PT	development of analgesics, anaesthetics and anti-addiction agents		
XX			
PS	Claim 8; Page -; 26pp; German.		
CC	This sequence encodes a novel human mu-opioid receptor in which a G		
CC	nucleotide at position 41 of the wild-type sequence represented in		
CC	AAV61984 is replaced by a T. The wild type receptor and its variants,		
CC	polymorphisms and mutants are used in a method for detecting		
CC	predisposition to disease, particularly addictive disease, by isolating		
CC	DNA from a sample, genotyping selected positions and comparing with a		
CC	reference DNA. Such sequences are used to develop analgesic,		
CC	anaesthetic, anti-addictive and psychopharmaceutical agents, to construct		
CC	genes and vectors, particularly for pharmaceutical development, to		
CC	develop diagnostic kits for predicting risk of addiction, response to		

Db 1321 agaacactagagaccaccctccagcgccaatacagtgatagaactaatcatcagctag 1380
 QY 1407 AAAATCTGAGAGAGAACTGCTCCCTGACCAAGGAGTTCATGCCATTCGACCTT 1466
 Db 1381 aaatctggaagagaactcgtcgttcgctcccaacagggtctcagcattccgacct 1440
 QY 1467 CACCAAGCTTAGAGCCACCATTATGTGAGAACGACGTTGCTTCAAGAAATGTGTAGAG 1526
 Db 1441 caccagcttagaagcaccatgtatgtgaaagcaggtctcacaagaatgtgtaagag 1500
 QY 1527 CTCTATTCTGAGAGAGGCTGCTTTAGGTCACTCAACCTCTTCTCTGAGCA 1586
 Db 1501 ctctaattctccttagaagaatgctcactcttaagtgatcacaacctctcctctgcca 1560
 QY 1587 CTCTGCTCTGACATTAGAGG 1607
 Db 1561 ctctgctctgacattagag 1581

RESULT 7
 AAV61987
 ID AAV61987 standard; cDNA; 2162 BP.
 AC AAV61987;
 DT 11-JAN-1999 (first entry)
 XX Human mu-opioid receptor cDNA variant 3.
 DE Human mu-opioid receptor cDNA variant 3.
 KM Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
 KW predisposition; addiction; analgesic; anesthetic; anti-addictive;
 KW psychopharmacological agent; diagnostic; side effect; drug; opiate;
 XX cocaine; inherited alcoholism; human; ss.
 OS Homo sapiens.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT CDS 213..2040
 FT /tag= a
 FT /product= "mu-opioid receptor"
 FT misc_feature 502..503
 FT /tag= b
 FT /note= "Site of Intron 1"
 FT misc_feature 855..856
 FT /tag= c
 FT /note= "Site of Intron 2"
 FT misc_feature 1376..1377
 FT /tag= d
 FT /note= "Site of Intron 3"
 FT mutation 102
 FT /tag= e
 FT /note= "Wild type C is replaced by T"
 XX WO9833937-A2.
 PN 06-AUG-1998.
 PD 02-FEB-1998; 98WO-DE00382.
 PF 03-FEB-1997; 97DE-1003925.
 PR (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
 PA Hoehe M, Wendel B;
 XX WPI; 1998-437487/37.
 DR New genomic and cDNA sequences encoding human mu-opioid receptor -
 PT used, e.g. to predict pre-disposition to addiction and for
 PT development of analgesics, anaesthetics and anti-addiction agents
 XX Claim 8; Page -; 26pp; German.

XX This sequence encodes a novel human mu-opioid receptor in which a C
 CC nucleotide at position 102 of the wild-type sequence represented in
 CC AAV61984 is replaced by a T. The wild type receptor and its variants,
 CC polymorphisms and mutants are used in a method for detecting
 CC predisposition to disease, particularly addictive disease, by isolating
 CC DNA from a sample, genotyping selected positions and comparing with a
 CC reference DNA. Such sequences are used to develop analgesic,
 CC anesthetic, anti-addictive and psychopharmacological agents, to construct
 CC genes and vectors, particularly for pharmaceutical development, to
 CC develop diagnostic kits for predicting risk of addiction, response to
 CC analgesics or anaesthetics, or development of side effects from a drug.
 CC Particular applications are used to determine risk of addiction to opiates or
 CC cocaine, or of developing inherited alcoholism.
 CC Note: This sequence is not represented in the specification and has
 CC been constructed from the wild-type sequence represented in AAV61984 in
 CC accordance with the specification.

XX
 SQ Sequence 2162 BP; 562 A; 564 C; 458 G; 576 T; 2 other;

Query Match 97.0%; Score 1561; DB 19; Length 2162;
 Best Local Similarity 99.6%; Pred No. 0;
 Matches 1575; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 28 TGGAGAGGGGCTATACGAGAGAGAAATGTCAGATGCTCAGCTCGCTCCCTCCGCTGA 87
 Db 1 tggagaggggcatatacagcagagagatgcatagctcagctcgtccctccgcctga 60

QY 88 CGCTCTCTCTGTCTCTACGACGAGCTGTTTCTGTAAAGAAACAGAGAGCTGTGACAC 147
 Db 61 cgtctctctctgtctctacgacagactggttctgttaagaaatagcagagcgtgtgacgc 120

QY 148 GGGGAAAGAGAGGCGCTGAGGCGCTTGAACCGGAAATCTCGGCTCGCTGACCT 207
 Db 121 ggcgaagagagagcgtgagcgttgagacccgaagatctcgtgtccctgactacct 180

QY 208 CGCAGAGC-GTGGCCGCGCGGCGGTGACATGACAGACAGAGCGCTGCCCCACAGAC 266
 Db 181 cgcagagcgggtgcccgcgcgcgtacatcagacagcagcgtgccccacagacg 240

QY 267 CCAGCAATTGACATGCTGCTTGGCGTACTCAAGTTGCTCCCGACAGCCAGCCGGTT 326
 Db 241 ccagcaattgactgtactgtcgttactcaagtgtctcccaagaccagcccggtt 300

QY 327 CCGGCTGCAACTGTCCGACTTAGATGGCAACCTGCGCACCCATGCGGTAACCGCA 386
 Db 301 ccgggtcaactgtgccacttagatggaacacctgtccgaaccaagcgtccgaaccgca 360

QY 387 CGGACCTGGGCGGAGAGAGAGCTGTGCTCCGACCGGAGTCCCTCCATGATCACGG 446
 Db 361 cgaacctggcgagagagcagcctgtgcccctcgaacgagtcctctcatgatacag 420

QY 447 CCATCAGCATGATGCCCTCTACTCATGCTGTGCGTGGGCGCTTTCGGAACCTTC 506
 Db 421 ccatacagatcatgcccctctactcatcgtgtgctgtggtggtctctcgaacctcc 480

QY 507 TGGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 566
 Db 481 tggtcatagtatgatatgatatgatatgatatgatatgatatgatatgatatgatatgatat 540

QY 567 TCAACCTTCTCTGCGAGATGCTTAGCCACCAAGTACCTGCGCTTCCAGAGTGAATT 626
 Db 541 tcaaccttctctgagatgctttagccacagatcaccctcctcagagtgtaatt 600

QY 627 ACCTAATGGGAACATGCGCATTTGGAACCATCTTTGCAAGATGATCTCATGATT 686
 Db 601 accataatgggaacatgcatcttggaacacatctcttgcaagatgattctcatagatt 660

QY 687 ACTATACATGTTTCCACCATATTCACCCCTGACCACTGAGTGTGATGATCATTTG 746
 Db 661 actataacatgtcacacagcatatccacctctgacatgagtgatgatacatatg 720

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QY 747 CAGTCTCCACCCCTGTGACAGGCTTATAGATTTCCCTACTCCCGGAATGCCAAATATATCA 806
    |||||||
Db 721 cagctctgcaacccctgtaagcccttagatttcgactcccggaatgccaataattca 780
QY 807 ATGCTGCAACTGATCTCTCTTCCAGCCATTTGGTCTTCTGTAATGTTTCAATGCTACAA 866
    |||||||
Db 781 atgtctgcaactgatactctctctcagccattgtctctcgttaattgtacatgctacaa 840
QY 867 CAAATATCAGGCAAGGTTTCAATGATGTAATGTAATCTCTCATCTCAACCAACCTGGTACT 926
    |||||||
Db 841 caaatacaaggaagcttccatagatctgtaacacaaactctccacacacccggtact 900
QY 927 GGGAAACCTGCTGAAGATCTGTGTTTTCATCTTCCGCTTCAATATGCAATGCTCATCA 986
    |||||||
Db 901 gggaaacccctgtaagatctgtttctatcttcgcttcattatgccaagtgctca 960
QY 987 TTACCGTGTGCTATGACTGATGATCTTGGCCCTCAAGAGTGTCCGATGCTCTGGCT 1046
    |||||||
Db 961 ttaccgtgtctatgactgatactctgcccacaaagtgctcgcagatgctcttgct 1020
QY 1047 CCAAGAAAGAGACAGATCTTGAAGGATCACAGAGTGTGCTGTGGTGGCTG 1106
    |||||||
Db 1021 ccaagaaagagacaggaactcttcgaagatcaccaagatggtgctggtggtctg 1080
QY 1107 TGTTCATGCTGTCTGTGACTCCCATTCATTCATTCATTCATTCATTCATTCATTCATTC 1166
    |||||||
Db 1081 tgttcactgctgtctggaactcccatcattacatctacatcattaaagccttggttcaaa 1140
QY 1167 TCCAGAAACTAGCTTCCACACTTCTTGGCACTTCTGCACTTCTGCTGCTGCTGCTGCTG 1226
    |||||||
Db 1141 tcccaagaactagcttccacagactgtctctgcaactctgcatgctctggttaccacaa 1200
QY 1227 ACAGCTGCTCAACCCAGTCTTATGATTCATTCATTCATTCATTCATTCATTCATTCATTC 1286
    |||||||
Db 1201 acagctgctccaaccccgcttcattatgacttctcgatgtaaaacttaaacgacttca 1260
QY 1287 GAGAGTTCTATGCCAAGCTTCTTCAACATTTGAGCAACAAACTCCATCGAATTCGTC 1346
    |||||||
Db 1261 gaaagtctgtatcccaactcttccacaacttgagcaacaaactccacatcgaattcgtc 1320
QY 1347 AGAAGACTAGAGCCACCCCTCCAGGCGCAATGAGTGAAGCAATATCATCAGCTAG 1406
    |||||||
Db 1321 agaagactagagacaccccccacgagccataacagtagagataacatacatcaagctag 1380
QY 1407 AAATCTGGAAGCAAGAACTGCTCCGTTGCCCTAACAGGCTCTCATGCCATTCGACCTT 1466
    |||||||
Db 1381 aaatctggaagcaagaaactgctccgttgccttaacaggttccatgctccagactt 1440
QY 1467 CACCAAGCTTAGAAGCCACCATGATGTGAGAGAGGTTGCTTCAGCAATGTGAGAGG 1526
    |||||||
Db 1441 caccaaagcttagaagccacatgattgtgaaagcaagttcttcaagaagtgtgtagag 1500
QY 1527 CTCTAATCTCTAGGAAGTGCCTGTTTAAAGTCAACCTTCTCTCTGCTGCGCA 1586
    |||||||
Db 1501 ctctaattctctggaagtgacctttagcattagcaccaccccttctctctgcca 1560
QY 1587 CTCTGCTCTGACATTAGAGG 1607
    |||||||
Db 1561 ctctgctctgacattagag 1581

```

RESULT 8

AAV61988 AAV61988 standard; cDNA; 2162 BP.

XX AAV61988;

XX 11-JAN-1999 (first entry)

XX Human mu-opioid receptor cDNA variant 4.

XX Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
 XX Predisposition; addiction; analgesic; anaesthetic; anti-addictive;

```

KW psychopharmaceutical agent; diagnostic; side effect; drug; opiate;
KM cocaine; inherited alcoholism; human; ss.
XX Synthetic.
OS Homo sapiens.
OS Synthetic.
FH Key 213..2040 Location/Qualifiers
FT CDS 213..2040 /tag= a
FT /product= "mu-opioid receptor"
FT misc_feature 502..503 /tag= b
FT /note= "Site of intron 1"
FT misc_feature 855..856 /tag= b
FT /note= "Site of intron 2"
FT misc_feature 1376..1377 /tag= d
FT /note= "Site of intron 3"
FT mutation 175 /tag= e
FT /note= "Wild type C is replaced by A"
FT FT
PN W09833937-A2.
PD 06-AUG-1998.
PF 02-FEB-1998; 98WD-DE00382.
PR 03-FEB-1997; 97DE-1003925.
PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
PI Hoehe M, Wendel B;
PI WPI; 1998-437487/37.
XX
XX New genomic and cDNA sequences encoding human mu-opioid receptor -
XX used, e.g. to predict pre-disposition to addiction and for
XX development of analgesics, anaesthetics and anti-addiction agents
XX
XX Claim 8; Page -: 26pp; German.
XX
XX This sequence encodes a novel human mu-opioid receptor in which a C
XX nucleotide at position 175 of the wild-type sequence represented in
XX AAV61984 is replaced by an A. The wild-type receptor and its variants,
XX polymorphisms and mutants are used in a method for detecting
XX predisposition to disease, particularly additive disease, by isolating
XX DNA from a sample, genotyping selected positions and comparing with a
XX reference DNA. Such sequences are used to develop analgesic,
XX anaesthetic, anti-addictive and psychopharmaceutical agents, to construct
XX genes and vectors, particularly for pharmaceutical development, to
XX develop diagnostic kits for predicting risk of addiction, response to
XX analgesics or anaesthetics, or development of side effects from a drug.
XX Particular applications are to determine risk of addiction to opiates or
XX cocaine, or of developing inherited alcoholism.
XX Note: This sequence is not represented in the specification and has
XX been constructed from the wild-type sequence represented in AAV61984 in
XX accordance with the specification.
XX
SQ Sequence 2162 BP; 563 A; 564 C; 458 G; 575 T; 2 other:

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Query Match 97.0%; Score 1561; DB 19; Length 2162;

Best Local Similarity 99.6%; Pred. No. 0; Matches 1575; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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QY 28 TGGAGAGGGGCTTATAGCAGAGAGAGATGTACATGCTGCTGCCCTCCGCTGA 87
    |||||||
Db 1 ttggagagggtatagcagagagagatgtacatgctgctgccctccgctga 60
QY 88 CGCTCTCTCTGCTGACGACGAGCTGTTTCTGTAAGAAACGAGGAGCTGTGGCAGC 147
    |||||||

```


PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.

PI Hoehe M, Wendel B;

DR WPI; 1998-437487/37.

PT New genomic and cDNA sequences encoding human mu-opioid receptor -
PT used, e.g. to predict pre-disposition to addiction and for
PT development of analgesics, anaesthetics and anti-addiction agents
XX
PS Claim 8; Page -: 26pp; German.

CC This sequence encodes a novel human mu-opioid receptor in which a C
CC nucleotide at position 229 of the wild-type sequence represented in
CC AAV61984 is replaced by an T. The wild type receptor and its variants,
CC polymorphisms and mutants are used in a method for detecting
CC predisposition to disease, particularly addictive disease, by isolating
CC DNA from a sample, genotyping selected positions and comparing with a
CC reference DNA. Such sequences are used to develop analgesic,
CC anaesthetic, anti-addictive and psychopharmaceutical agents, to construct
CC genes and vectors, particularly for pharmaceutical development, to
CC develop diagnostic kits for predicting risk of addiction, response to
CC analgesics or anaesthetics, or development of side effects from a drug.
CC Particular applications are to determine risk of addiction to opiates or
CC cocaine, or of developing inherited alcoholism.
CC Note: This sequence is not represented in the specification and has
CC been constructed from the wild-type sequence represented in AAV61984 in
CC accordance with the specification

50 Sequence 2162 BP; 562 A; 564 C; 458 G; 576 T; 2 other;

Query Match	97.08;	Score 1561;	DB 19;	Length 2162;
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Best Local Similarity 99.68; Pred. No. 0;

Matches 1575; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

OY	28	TGGGAGGGGGCGCTATACCGAGAGGAGGAATGTACAGTATGCTACAGCTGGAGTCCCTCCGCGCTGA	87
Db	1	tgggaaggggggtctaaacgaagaggaatgltcaatgtccacagcttcggtccctccgcgtga	60
OY	88	CGCTCTCTCTGTGTCTAG6CCAGGAGCTGGTTTCTGTAA6AAACAGACAGAGCTGTGGAGC	147
Db	61	cgctctctctctgtcttcacgaagactggttctctgtaagaacacagcagagctgtggaagc	120
OY	148	GGCGAAAGGAAGCGGCGTGAAGCGCTTGGAAACCGGAAAAGTCTGTGCTCTCTCGCTAAGCT	207
Db	121	ggcgaaaggaagcggcttgaaggcgcttggaaacccgaaagtcgtgtctcctgctactc	180
OY	208	CGCAGACG - GAGCCCGCCCGCCGCTGCAGTACCAATGAGACAGAGCGGTGCCCCAGAGACG	266
Db	181	cgcacagagcggccgcgcgcgcgtccagtlcaacagagacagcagcgtctccaccgaagc	240
OY	267	CCAGCAATTTGCACGTATGCTTTGGCGTACTCAATTTCTCTCCAGCAACCGACCGCCGTT	326
Db	241	ccagcaatltgacactgtagccttcggtctactcaagltgtctccccaagcccaagcccggtc	300
OY	327	CTGTGGGTCAACTTGTCCCACTTAGATGGCAACCTGTCCGACCCATGCGGTCGGAACCGCA	386
Db	301	cctgtgtcaacttgtcccaacttagatgcaacactgtccgagccactgtggtcggaaacgca	360
OY	387	CCGACACTGGGCGGGAGAGACAGCTGTGCTCCCTCCGACCGGCAGTCTCTCATGATACGG	446
Db	361	ccaacacttggcggggaagagacagcctgtgacctccgacccgagtcctccatgatacagc	420
OY	447	CCATCAGCATATGCGCCCTACTCCATCGTGGTCCGGTGGGGGCTTTGGGAAACTTC	506
Db	421	ccaatcaagatcatgtgcccctcaaccatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	480
OY	507	TGGTCATGTATGTATTGTGCAGATACACCAAGATGAAGACTGGCCACCAATCTACATT	566
Db	481	tgtgtcatgtatgtatgtgtcaataacccaagatgtaagactgtccaaccaatcatcaattc	540
OY	567	TCAACCTTGGCTCTGGAGATGCCCTTAGCCACCAAGTACCCCTCCAGAGTGTGAATT	626

Db	541	tcaacctgtcctctgagcaatgaccttgagccaccagtaacctgtccctccagagtgtgaatt	600
OY	627	ACCTAAATGGACAATGGCCATTTTGGAAACATCTCTTGGACAGATAGTGATCTCCATAGATT	686
Db	601	acctaatgagaaatctgagcaatcttggaaccaatctcttgcaagaatagatcatccaatagatt	660
OY	687	ACTTAAACATATTACACGAGATATTACCTTGACACCTTGACACCATGATGTTGATCATGATTG	746
Db	661	actatacaatgttcaaccagatatactcaacctctgcagccaatgagtgtgtatgtaatacatgt	720
OY	747	CAGTCTGCCACCTGTCAAGGACCTTAGATTCCGTACTCCCGAAATGGCCAAATTAATATCA	806
Db	721	cagctgcaccacctgtaagaagccttagattcttcgtaactcccgaaatgtccaaatattatca	780
OY	807	ATGTCGTGAACATGGATCTCTCTTTCAGGCCATTGGTCTCTCTGTAATGTTCAATGGGCTACAA	866
Db	781	atgtctgaaactgtgaatccctctctctcagccaattgtcttccgttaatgtltcaatgtctacaa	840
OY	867	CAAAATACAGGCAAGTTCATAGATTGTACACTAAACATTCTCTCATCCACACCTGGTACT	926
Db	841	caaaatcaagcaaggtlccatagattgtatacaatacatctctctcatccaacacctgtact	900
OY	927	GGGAAACCTGCTCAACATCTGTGTTTTCATCTTGGCCTTCAATTAAGCCAGTGTCATCA	986
Db	901	gggaaaacctctgtgaagaatctctgttttcttctcaatcttcgcttcatatagccagtgccatca	960
OY	987	TTACCGTGTGCTATGACATGATATCTTGGCCTCAAGAAGTGTCCGATGCTCTGTGCT	1048
Db	961	ttaccgtgtgtatgagactgtatgactcttgagcttcaagagtgtccgacatgtctctgtcct	1020
OY	1047	CCAAGAAGAAAGACAGCAATCTTCGAAAGATCAACGAGATGGTGGTGGTGGTGGTGGCTG	1106
Db	1021	ccaaagaaagaaagaaacatctcttcgaagaatccaggaatgagtgctggagtgagtgagctg	1086
OY	1107	TGTTTCACTGCTGTGCTGACATCTCCATTCCACATTTTACCTCATCTTAATAAGCCTTGTTACAA	1166
Db	1081	tgtttcactgtctgtgtgagcttcccatccaattagctcatcaatlaaagcttgtttacaa	1140
OY	1167	TCCCAAGAACTACGTTTCCACAGCTTTTCTTGGACATTCCTGCATGTGCTTAGAGTTACACA	1222
Db	1141	tcccagaaactacgtlcttcacagctgttctctgtgcacttcgtcatctgactaagttacaa	1200
OY	1227	ACACCTGCTCTCAACCCAGTCTCTTATGACATTTCTGGATCAAAAATCTCAACACATGCTTCA	1286
Db	1201	acagctgtctcaaacaccagttccttattgcaattctctgtgaatgaaaacttcaaaagatgtctta	1260
OY	1287	GAGAGTTCTGTATCCCAACCTCTTTCCAACATTAGCAACAAAATCTGCACATTCGATTGCTC	1346
Db	1261	gagagttctgtatctccaaactcttccaacattgagaanaaaaacttccactctgaattctgc	1320
OY	1347	AGAACACTAGAGACACACCTCTCCACGGCCAAATCACTGATAGAACTAATCATCACTAGCTAG	1406
Db	1321	agaaactatagagacacacctccaagggccaatactagtatgaactaaatcatcatcagctag	1380
OY	1407	AAAAATCTGAGAGCAGAAATCTGTCCTGTGGCTTAACAGGGCTCATGCCATTCCGACCTT	1466
Db	1381	aaaactctggaagcagaacatgtctcgtgtgccttaacaaggtctcatgtccattccgaactt	1440
OY	1467	CACCAACCTTAGAAGCCACCATGTATGTGGAAACAGCTTGCTTCAAGAAATGTGTGAGAG	1526
Db	1441	caaccaagcttagaagccacaatgtatgtgaaacaggtgtgtctcaagaagtgtatgtagaggg	1500
OY	1527	CTCTAAATTTCTTAGGAAATGCTCTGCTTTTATGAGTCAATCCAACTCTTTCCTCTGAGCCA	1586
Db	1501	ctctaaattctctaggaagtgctactactttagtgaatccaacctcttccctctctgagca	1560
OY	1587	CTCTGCTCTGCACATTAGAGG 1607	
Db	1561	ctctgctctctgcacatttagag 1581	

RESULT 10

AAV61990
 ID AAV61990 standard; cDNA; 2162 BP.
 XX
 AC AAV61990;
 XX
 DT 11-JAN-1999 (first entry)
 XX
 DE Human mu-opioid receptor cDNA variant 6.
 XX
 KW Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
 KW predisposition; addiction; analgesic; anaesthetic; anti-addictive;
 KW psychopharmaceutical agent; diagnostic; side effect; drug; opiate;
 KW cocaine; inherited alcoholism; human; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PH Key Location/Qualifiers
 FT CDS 213..2040
 FT /tag- a
 FT /product= "mu-opioid receptor"
 FT 502..503
 FT /tag- b
 FT /note= "Site of intron 1"
 FT 855..856
 FT /tag- c
 FT /note= "Site of intron 2"
 FT 1376..1377
 FT /tag- d
 FT /note= "Site of intron 3"
 FT 330
 FT /tag- e
 FT /note= "Wild type A is replaced by G"
 XX
 PN W09833937-A2.
 PD 06-AUG-1998.
 XX
 PF 02-FEB-1998; 98WO-DE00382.
 XX
 PR 03-FEB-1997; 97DE-1003925.
 XX
 PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
 XX
 PI Hoehe M. Wendel B;
 DR MPI; 1998-437487/37.
 XX
 PT New genomic and cDNA sequences encoding human mu-opioid receptor -
 PT used; e.g. to predict pre-disposition to addiction and for
 PT development of analgesics, anaesthetics and anti-addiction agents
 XX
 PS Claim 8; Page -: 26pp; German.
 XX
 CC This sequence encodes a novel human mu-opioid receptor in which an A
 CC nucleotide at position 330 of the wild-type sequence represented in
 CC AAV61984 is replaced by a G. The wild type receptor and its variants,
 CC polymorphisms and mutants are used in a method for detecting
 CC predisposition to disease, particularly addictive disease, by isolating
 CC DNA from a sample, genotyping selected positions and comparing with a
 CC reference DNA. Such sequences are used to develop analgesic,
 CC anaesthetic, anti-addictive and psychopharmaceutical agents, to construct
 CC genes and vectors, particularly for pharmaceutical development, to
 CC develop diagnostic kits for predicting risk of addiction, response to
 CC analgesics or anaesthetics, or development of side effects from a drug.
 CC Particular applications are to determine risk of addiction to opiates or
 CC cocaine, or of developing inherited alcoholism.
 CC Note: This sequence is not represented in the specification and has
 CC been constructed from the wild-type sequence represented in AAV61984 in
 CC accordance with the specification.
 XX
 SO Sequence 2162 BP; 561 A; 565 C; 459 G; 575 T; 2 other;

Query Match 97.0%; Score 1561; DB 19; Length 2162;
 Best local Similarity 99.6%; Pred. No. 0;
 Matches 1575; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 28 TGGGAGGGGGCTATACGACAGAGAGATGTCAGATGCTCAGCTCCCTCCGCTTA 87
 DB 1 tgggagggggtatacagcagagagatgtcagatgtcagctcgtccctccgctga 60
 QY 88 CGCTCCCTCCTCTCTCAGCAGGAGCTGTTTCTGTAAAGAGAGAGAGAGAGAGAG 147
 DB 61 cgtctccctctctctcagcagagagctgttctgtlaagaaagagagagagctgtgcagc 120
 QY 148 GGGGAAAG 207
 DB 121 ggcgaaag 180
 QY 208 CGCAGAGC-GTCCCGCCCGCCCGCCGTCAGTACATGAGACAGAGAGAGAGAG 266
 DB 181 cgcacagcgggtgc 240
 QY 267 CGAGCAATTGCACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 326
 DB 241 ccagcaattgcactgactgtgctgtgctgctgctgctgctgctgctgctgctgctg 300
 QY 327 CTTGGTCAACTTGTCCCACTTGTAGTGCACCTGTCCGACCATCGGTGCGAACCGCA 386
 DB 301 cctgggtcaactgtgtcccaactgtgtgactgactgactgactgactgactgactgactg 360
 QY 387 CCGACCTGGCGGGAG 446
 DB 361 ccaactggcgaggag 420
 QY 447 CCATCAAGATCATGAGCGCTCTACTCATGCTGTGCTGCTGCTGCTGCTGCTGCTGCT 506
 DB 421 ccatcaagatcatgagcgcctctactcatgctgtgctgctgctgctgctgctgctgctg 480
 QY 507 TGGTCATGTATGTATGTATGTATGTATGTATGTATGTATGTATGTATGTATGTAT 566
 DB 481 tggtcattgtatgtatgtatgtatgtatgtatgtatgtatgtatgtatgtatgtat 540
 QY 567 TCAACCTGTGCTGTGCGAGATGCTTGTGCGACAGTACCTGCTTGTGAGAGTGAATT 626
 DB 541 tcaacctgtgctgtgctgtgctgtgctgtgctgtgctgtgctgtgctgtgctgtgct 600
 QY 627 ACCTAATGGGAATGAGGCACTTGTGAACCATCTTGTGAAGATGATGATGATGAT 686
 DB 601 acctaatgggaatgagggcaacttgtgaaccatcttgtgaagatgattgattgattgatt 660
 QY 687 ACTATACATGTTTCACACAGCATATTCACCTGTGACCATGAGTGTGTGATGATGAT 746
 DB 661 actataacatgttcacacagcatatttcacctgtgacccatgagtgatgtgtgattgatt 720
 QY 747 CAGTGTGCCACCTGTGACAGGCTTGTAGATTTCGTTACTCCCGCAAAATGCAAAATTATCA 806
 DB 721 cagtgtgccacctgtgacaggctttagatttccgttactcccgcaaatgcaaatatlatca 780
 QY 807 ATGTGTGCAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 866
 DB 781 atgtgtgcaactgattgattgattgattgattgattgattgattgattgattgattgatt 840
 QY 867 CAATAACAGGAGAGGTTCCATGATGATGATGATGATGATGATGATGATGATGATGAT 926
 DB 841 caataacaggagagggttccatgattgattgattgattgattgattgattgattgattgatt 900
 QY 927 GGGAAAACCTGCTGAGAGATCTGTGTTTTCATCTTCCCTTTCATTTAGCAGAGTCTATCA 986
 DB 901 gggaaaacctgctgagagatctgtgttttcattcttcccttccatattagcagagtgctatca 960
 QY 987 TTACCGTGTCATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1046
 DB 961 ttaccgtgtcatgtagacgtatgattcttgcctcaagaagtgttcgcatgtctctgcgt 1020

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QY 1047 CCAAGAAAAGAGAGAAATCTTGAAGATACACAGATGCTGCTGGTGGCTG 1106
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QY 1107 TGTTCATCGTGTGAGCTCCCATTCATTTACGATTCATTTAAAGCTTGGTTACAA 1166
DB 1081 tgttcattgctgtgagctccattcacattacgtatcatlaaagccttgglttaaa 1140
QY 1167 TCCGAGAACTAGCTTCCAGACTGTTTCTTGACACTTCGATTCGCTTAGCTTACACAA 1226
DB 1141 tccagaagaactagatccagctgttcttgagccttctgcatgctcctgaagtaacaa 1200
QY 1227 ACAGCTGCTCAACCCAGTCTTTATGCAATTCGTGATGAAGAACTTCAACGATGCTTCA 1286
DB 1201 acagctgctcaaccagctccttattgatttctgtagaagaactccaacgaltgttca 1260
QY 1287 GAGAGTTCGTATCCCAACCTTCCAAACATTTAGCAACAAACTCCCTGATGATGCTC 1346
DB 1261 gagagttctgtatcccaaccttccaaatlgagcaacaactccaactcgaattcgtc 1320
QY 1347 AGAACACTAGAGACCACCCCTCCACGGCCATACAGTGAAGAACTATCATGACTAG 1406
DB 1321 agaactacagagaccacaccccccacagccaaatagatgtagaactaatcatcagctag 1380
QY 1407 AAAATCTGGAAGACAGAAACTGCTCCGTTGCCCTTAACAGGCTCATGCCATTCGACCTT 1466
DB 1381 aaatctggaagacgaactctccgttgccttaacagaggtcatcgtccatccgaactt 1440
QY 1467 CACCAAGCTTGAAGCCCACTGATGGAAGAGGTTGCTTCAAGAAAGTGTAGAGAG 1526
DB 1441 caccagaactagaagccacatgtagtgaagcaggttcttcaagaatgtagtagaag 1500
QY 1527 CTCTAATCTCTAGAAAGTCCCTGCTTTTATGATCATCAACCTTCTCTCTGGGCA 1586
DB 1501 ctctaattctctagaaagtgctactttagtcatcccaaccttccctcttgagca 1560
QY 1587 CTCTGCTCTGCACATTAGAGG 1607
DB 1561 ctctgctctgcacattagaag 1581

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RESULT 11

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ID AAV61991 standard; cDNA; 2162 BP.
XX
AC AAV61991;
XX
DT 11-JAN-1999 (first entry)
XX
DE Human mu-opioid receptor cDNA variant 7.
XX
KM Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
KM predisposition; addition; analgesic; anaesthetic; anti-addictive;
KM psychopharmaceutical agent; diagnostic; side effect; drug; opiate;
KM cocaine; inherited alcoholism; human; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 213..2040
FT FT /tag- a
FT FT /product- "mu-opioid receptor"
FT FT misc_feature /tag- b
FT FT /note- "Site of intron 1"
FT FT misc_feature /tag- c
FT FT /note- "Site of intron 2"
FT FT misc_feature /tag- d
FT FT /note- "Site of intron 3"
FT FT mutation 666

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PT FT /tag= e
FT FT /note= "Wild type A is replaced by G"
PN PN
PN MO9833937-A2.
PD PD
PD 06-AUG-1998.
PF PF
PF 02-FEB-1998; 98WO-DE00382.
PR PR
PR 03-FEB-1997; 97DE-1003925.
PI PI
PI (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
PI Hoehe M, Wendel B;
PI WPI; 1998-437487/37.
PT PT
PT New genomic and cDNA sequences encoding human mu-opioid receptor -
PT used, e.g. to predict pre-disposition to addiction and for
PT development of analgesics, anaesthetics and anti-addiction agents
PS PS
PS Claim 8; Page -: 26pp; German.
XX XX
XX This sequence encodes a novel human mu-opioid receptor in which an A
XX nucleotide at position 666 of the wild-type sequence represented in
XX AAV61984 is replaced by a G. The wild type receptor and its variants,
XX polymorphisms and mutants are used in a method for detecting
XX predisposition to disease, particularly addictive disease, by isolating
XX DNA from a sample, genotyping selected positions and comparing with a
XX reference DNA. Such sequences are used to develop analgesic,
XX anaesthetic, anti-addictive and psychopharmaceutical development, to
XX genes and vectors, particularly for pharmaceutical development, to
XX develop diagnostic kits for predicting risk of addiction, response to
XX analgesics or anaesthetics, or development of side effects from a drug.
XX Particular applications are to determine risk of addiction to opiates or
XX cocaine, or of developing inherited alcoholism.
XX Note: This sequence is not represented in the specification and has
XX been constructed from the wild-type sequence represented in AAV61984 in
XX accordance with the specification.
XX
XX Sequence 2162 BP; 561 A; 565 C; 459 G; 575 T; 2 other;

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Query Match 97.0%; Score 1561; DB 19; Length 2162;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1575; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

```

QY 28 TGGAGGGGGGCTATACGACAGAGAGAAATGTCAGTGTCTAGCTGCCCTCCGCTGA 87
DB 1 tggagggggggtacacgacagagagaaatgtcagatgtctagctgctccctcgcctga 60
QY 88 CGCTCCTCTCTGCTTCAGCCAGGACTGTTTCTGTAAAGAAAGACAGAGCTGTGGCAGG 147
DB 61 cgtctcctctgtctcagccaggaactgttctgtgaagaacagcagagctgtgagcag 120
QY 148 GCGCAAGAGAGCGGCTGAGGCGCTTGAACCCGAAAGTCTCGTGCCTCTGAGTACT 207
DB 121 ggcgaagaagagcggtcgtgagcgcttgaacccgaaagctcgtctctgtctacct 180
QY 208 CGCACAGC-GTGCCCGCCGCGGCTCAGTACATGACACAGAGCGTGGCCCAAGC 266
DB 181 cgcacagcggtgtccgcgcgcgcgtacatgacagcagcgcgtgcccccaagcag 240
QY 267 CCAGCAATTCAGTATGATGCTTGGCGTACATCAAGTCTCTCCAGCACCAGCCCGGTT 326
DB 241 ccagcaattgcatgacgtacctgtggtcgtacccaagtgtctcccaagcaccagccggtt 300
QY 327 CTTGGGTCAACTTGTCCCACTTAGATGGAACCTGTTCGACCCATGGGTGCGAACCGCA 386
DB 301 cctgggtcaacttgttcccaacttagatggaacctgttcgacccatgggtgctcgaaacgca 360
QY 387 CCGACTGGGCGGGAGACAGCCTGTGCTCCGACCGGACAGTCCCTCATATACAGG 446
DB 387 ccgactgggcgggagacagcctgtgctccgacccggacagtcctcatatcacagg 446

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Db 361 ccaacctggcgagagagacagctgtgccctcccgaccgagctcccatcatgacag 420
 QY 447 CCATCAGATCATGAGCCCTCTACTCCATCGTGGCTGGGGGCTCTTGGAACTTCC 506
 Db 421 ccatcagatcatgagccctctactccatcgtggtggcgccctccgaaactcc 480
 QY 507 TGGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 566
 Db 481 tggatcatgattgattgattgattgattgattgattgattgattgattgattgatt 540
 QY 567 TCACCTTGTCTGTGAGATGCTTGGCCACGAGTACCTGCCCTTCCAGAGTGAAT 626
 Db 541 tcaacctgtctgtgagatgcttggccacagtagtacctgtccctccagagtgta 600
 QY 627 ACCTAATGGACATGGCATTTGGAACTTGGAACTTGGAACTTGGAACTTGGAACT 686
 Db 601 accatattggaacatgagccatcttggaacatctcttggaagatagatgagat 660
 QY 687 ACTATACATGTTACACGATATTACCCCTTGCACACATGAGTGTGATGATGATG 746
 Db 661 actatgacatgttaccagacatattaccctctgcacacatgagtgatgacat 720
 QY 747 CAGTCCGACACCTGTGAGAGGCTTGAATTCCTGCTACTCCGGAATGGCAAAATTATCA 806
 Db 721 cagctgcacacctgtcaagaccttagatcttccgtactcccccgaatgtccaaat 780
 QY 807 ATGTCTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 866
 Db 781 atgtctgcaatgagatgagatgagatgagatgagatgagatgagatgagatg 840
 QY 867 CAAATATCAGGCAAGGTCATAGATTTGATACATTAATTCATTCATTCATTCAT 926
 Db 841 caaataacagcaaggttccatagattgtacatacattctctccatccacactgt 900
 QY 927 GGGAAACCTGTGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 986
 Db 901 gggaaacctgtgagatgagatgagatgagatgagatgagatgagatgagat 960
 QY 987 TTACCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1046
 Db 961 ttaccgtgtgcatgagatgagatgagatgagatgagatgagatgagatgag 1020
 QY 1047 CCAAGAAAAAGCAGAGATTTTCGAGAGATCAGCAGATGCTGCTGCTGCTGCT 1106
 Db 1021 ccaaaagaaaagcagagatcttcgagagatcaccagagatgctgctgctgct 1080
 QY 1107 TGTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1166
 Db 1081 tgttcacgtctgctgctgctgctgctgctgctgctgctgctgctgctgctg 1140
 QY 1167 TCCAGAACTACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1226
 Db 1141 tccagaaactacgctgctgctgctgctgctgctgctgctgctgctgctgctg 1200
 QY 1227 ACAGCTGCTCAACCGATGCTTTATGATTTCTGATGATGATGATGATGATGAT 1286
 Db 1201 acagctgctcaacccagctcttcatgcttctgagatgaaactcaaaagtg 1260
 QY 1287 GAGAGTTTGTATCCCACTCTTCCACATGAGCAACAAAATTCACATCGATTCGTC 1346
 Db 1261 gagagtttctgatacccaactcttccaacatgagaaacaaactccactcgat 1320
 QY 1347 AGAAGCTAGAGACACCCCTCCAGCGCAATACATGATGATGATGATGATGATGAT 1406
 Db 1321 agaaacttagagacacccctccacagccaatacagtgatgataactatcatcag 1380
 QY 1407 AAAATTTGAGACGAGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1466
 Db 1381 aaaatctggaagagaaactgctgctgctgctgctgctgctgctgctgctgct 1440
 QY 1467 CACCAAGCTTAGAAGCCACCATGATGATGATGATGATGATGATGATGATGATGATGAT 1526
 Db 1441 caccagcttagaagccacacatgatagtgagagagtgcttcaagaatgtgtagag 1500

QY 1527 CTCATATCTCTAGAAAGTGCCTGCTTTAGTCAATCCAACTCTTCTCTGAGCA 1586
 Db 1501 cctaatcttcaggaaagtgctactattagttacatccaactcttccctctgcca 1560
 QY 1587 CTCCTGCTGACATTTAGAGG 1607
 Db 1561 cctctgctgcacatlagag 1581

RESULT 12
 AA61992
 ID AA61992 standard; cDNA; 2162 BP.
 XX
 AC AA61992;
 XX
 DT 11-JAN-1999 (first entry)
 XX
 DE Human mu-opioid receptor cDNA variant 8.
 XX
 KW Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
 KW prediosition; addiction; analgesic; anaesthetic; anti-addictive;
 KW psychopharmaceutical agent; diagnostic; side effect; drug; opiate;
 KW cocaine; inherited alcoholism; human; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 FH Key
 FT CDS
 FT 213..2040
 FT /tag= a
 FT /product= "mu-opioid receptor"
 FT misc_feature
 FT 502..503
 FT /tag= b
 FT /note= "Site of intron 1"
 FT misc_feature
 FT 855..856
 FT /tag= c
 FT /note= "Site of intron 2"
 FT misc_feature
 FT 1376..1377
 FT /tag= d
 FT /note= "Site of intron 3"
 FT mutation
 FT 1006
 FT /tag= e
 FT /note= "Wild type G is replaced by A"
 PN W09833937-A2.
 PD 06-AUG-1998.
 XX
 PF 02-FEB-1998; 98WO-DE00382.
 XX
 PR 03-FEB-1997; 97DE-1003925.
 XX
 PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
 PI Hoehe M, Wendel B;
 XX
 DR WPI: 1998-437487/37.
 XX
 PT New genomic and cDNA sequences encoding human mu-opioid receptor -
 PT used, e.g. to predict pre-disposition to addiction and for
 PT development of analgesics, anaesthetics and anti-addiction agents
 XX
 PS Claim 8: Page -: 26pp; German.
 XX
 CC This sequence encodes a novel human mu-opioid receptor in which a G
 CC nucleotide at position 1006 of the wild-type sequence represented in
 CC AA61984 is replaced by an A. The wild-type receptor and its variants,
 CC polymorphisms and mutants are used in a method for detecting
 CC predisposition to disease, particularly addictive disease, by isolating
 CC DNA from a sample, genotyping selected positions and comparing with a
 CC reference DNA. Such sequences are used to develop analgesic,
 CC anaesthetic, anti-addictive and psychopharmaceutical agents, to construct

Db 661 actataacatgttaccagacataatcaacctctgcacccatgagtgctgatacatatg 720
Oy 747 CAGTCTGCCACCCCTGTCAGAGGCTTTCAGATTTCCTGATCTCCCGAAATGCCAAATATATCA 806
Db 721 cagctcgcacccctctcgaagccttagatcttcgtaactcccgaaatgcaaatatcata 780
Oy 807 AATGTGCAACGTGATCTCTCTTCAGCCATTGGTCTTCTGTAATGTTTCATG3GCTACAA 866
Db 781 atgtctgcacatgcatcctctctcagccatctgctctcgttaatgctcgtacaa 840
Oy 867 CAAATACAGCAGAGTTCATAGATTGTACATACTTCATCTCATCCAACTGGTACT 926
Db 841 caaaaacagcaaggttccatagatctgtaacatacattccatacctaactgttact 900
Oy 927 GGGAAACCTGCTGAAGATCTGTGTTTTCATCTGCGCTTCAATTATGCGAGTGCATCA 986
Db 901 gggaaaacctgtgaaagatctgttlttactcttcgctccttaataagccagtgctcata 960
Oy 987 TTACCGTGTGATGAGTATGATGATCTTGGCCTCAAGAGTCCGATGCTCTGAGCT 1046
Db 961 ttaacgtgtcctagatgactgactgactgactgactgactgactgactgactgactgact 1020
Oy 1047 CCAAGAAAGACAGAGATCTTCAGAGATCACCAGATGGTGGTGGTGGTGGTGGTGGTGG 1106
Db 1021 ccaaaagaaagacaggaatcttcgaagatcaaccaagatggtgctgctgctgctgctgctg 1080
Oy 1107 TGTTCATCTGCTGAGTATGATGATCTTCATCTGATCTTCATCTGATCTTCATCTGATCT 1166
Db 1081 tgttcatctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 1140
Oy 1167 TCCCAAGAACTAGCTTCAGAGTGTTCCTGACATCTTCATCTGATCTTCATCTGATCTTC 1226
Db 1141 tcccaagaaatcatctcagactgctgctgctgctgctgctgctgctgctgctgctgctgctg 1200
Oy 1227 ACAGTGGCTTCAGACCCAGTCTTATGATCTTCGATGATAAAACTTCAACAGATGCTTCA 1286
Db 1201 acagctgctcacaacccagctccttctgacttctgactgactgactgactgactgactgact 1260
Oy 1287 GAGAGTTCTGTATCCCAACCTTTCACATTCAGATGAGCAACAAATCCAGTTCGATCTGCTC 1346
Db 1261 gtagagttctgtatcccaacctcttccaaacttgagcaacaaactccactcgaattcgtc 1320
Oy 1347 AGAACATGAGAGACCAACCCCTCCACGGCCCAATACAGTGTGATGAACTAATCATCATGCTAG 1406
Db 1321 agaacactagagacacacccctccacagcccaatatacagtagataactaatcaatcaagctag 1380
Oy 1407 AAAATCTGGAACAGAAACTGCTCGTTCGCTTACAGAGGCTTCATGCGATTCGACACTT 1466
Db 1381 aaaacttgaaagcagaatactgctcgttgccttaacagaggtctcattcgaactcgaact 1440
Oy 1467 CACCAAGCTTAGAGCCACATGTATGTGAAGCAGGTTGCTTCAAGATGTGTAGGAGG 1526
Db 1441 caccagaacttagaagcaccacatgatatggaagcaggtgtcctcaagaatctgtaagaag 1500
Oy 1527 CTCTAATTCCTAGAGAAATGCTGCTTTTATGATCATCCAACTCTTTCCTCTGCGCA 1586
Db 1501 ccttaattctctaggaagaatgctcactttagtagtaactcaactcttctcctctcgtgcca 1560
Oy 1587 CTCTGCTCTGCACATTAGAGG 1607
Db 1561 ctctgctctgcacattagag 1581

RESULT 15
AAO93102
ID AAO93102 standard: cDNA; 2160 BP.
XX
AC AAO93102;
XX
DT 11-DEC-1995 (first entry)
XX
DE Human mu opiate receptor cDNA.
XX

KW Mu opiate receptor; hMOR; opiate agonist; opiate antagonist;
KM drug abuse; analgesic; ds.
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT CDS 213..1415
FT /*tag= a
PN
XX
XX MO9520667-A1.
PD 03-AUG-1995.
XX
XX 30-JAN-1995; 95WO-US01144.
XX
XX 28-JAN-1994; 94US-0188275.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX (USSH) US SEC DEPT HEALTH.
XX
XX Johnson PS, Persico AM, Uhl G, Wang J;
XX
XX WPT: 1995-275452/36.
XX
XX P-PSDB; AAK76780.
XX
XX New DNA encoding human mu opiate receptor - used esp. for screening
XX cpds. for activity as opiate agonists or antagonists
XX
XX Claim 4; Page 24-25; 49pp; English.
XX
XX hMOR cDNA was obtd. from a human cerebral cortical cDNA library
XX screened with fragments of a rat mu opiate receptor. Cloned hMOR
XX cDNA can be used as probes to examine the structure and function of
XX hMOR genes or to screen individuals for susceptibility to drug
XX abuse. Expression in e.g. COS cells allows production of
XX recombinant hMOR.
XX
XX Sequence 2160 BP; 563 A; 566 C; 455 G; 576 T; 0 other;
SQ

Query Match 96.5%; Score 1553; DB 16; Length 2160;
Best Local Similarity 99.6%; Fred. No. 0;
Matches 1567; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Oy 36 GGCTTTACGACAGAGAGATGTCAGATGCTGACGTCGCTCCGCTGACGCTCCTC 95
Db 9 ggcataagcagaagaaatgcaatgctcagctcgttccctcgtcctgagctctc 68
Oy 96 TCTGTCTCAGCCAGAGACTGCTTCTGTAAAGAAACAGAGAGCTGTGACGGCGAAAG 155
Db 69 tctgtctcagccagagactggttctcgttaagaaacagcagagctgtgcaagcggaag 128
Oy 156 GAAGCGGCTGAGGCGCTTGGAACCGGAAAGTCTGTGCTCTCTGCTTACTTCGACAGC 215
Db 129 gaagcgctgagagcgcttggaacccgaaatctcgtgtcctcgtcactcgcacagc 188
Oy 216 -GTGCCGCGCGCGGTGATGATGAGCAGACAGCGTGCAGGCGGCGGCGGCGGCGGCGG 274
Db 189 ggtgccgcgcgcgcgtcagtaacatgtaacagcagcgtctgcccccaagaaagccagcaat 248
Oy 275 TGCATGATGCTTGGCGTACTCAAGTTGCTCCGACAGCAGCCGCGGTTCTGCGGCTC 334
Db 249 tgcactgatgctgtgctgactcaagttgctcccgagcaccagcccggttctcgtgctc 308
Oy 335 AACTGTGCCACTTATGATGAGCAACTGTGTCGACCCATGCGGTGCGAACCGGACGACTG 394
Db 309 aactgtgccactttagatgcaactgttcgaccatcggttcgaaacgcacaaactg 368
Oy 395 GCGGAGAGACAGCCTGCGCTCCGACCGGAGTCTCCATGATGACGGCGCATCAG 454
Db 369 ggcggagagagaagcctgtgctcctcgcagcgaatcctcctcatgatacagcacaagc 428
Oy 455 ATCATGCGCCCTCTACTCATCATGCTGTGCGGCTTTCGGAACCTTCTGTGATG 514

Db 429 atcatggcccttaccatccatcgltgctggtggtccttcggaaaccttcctggtcatg 488
OY 515 TATGTGATTTGTGAGATACACCAAGATGAGACGTGCCACCAACTTACATTTCACCTT 574
Db 489 tatgtgtatgtcagatcaccaagaatgaagactgcccacacatctacatcttcaacctt 548
OY 575 GCTGTGACAGATGCGTTAGCCACAGTACCTGCGCTTCAGAGTGTGAATTAATCTATG 634
Db 549 gctctggcaatgacctagcaccagtaacctgacctccagagtgtgaattacctatg 608
OY 635 GGAACATGGCCATTGGAACCACTTTGCAAGATAGTATCTCCATAGATTACTATAC 694
Db 609 ggaacatggccatttgaacacatcttgcgaagtagtattccatagattactataac 668
OY 695 ATGTTACACAGCATATTCACCCCTCTGCACCATAGTGTGATGATATTCGAGTCTGC 754
Db 669 atgttccacagcatatcacacctctgcacatgagtgtgatcgtatcatgtcagtlctgc 728
OY 755 CACCCTGTCAAGGCGTTAGATTTCGGTACTCCCGAATGCCAAATTTATCAATGTCTGC 814
Db 729 caccctgtcaaggccttagatcttcgtaacctcccgaaatgcgcaaatatcatatgtctgc 788
OY 815 AACTGATCTCTCTTACGCACTTGTCTTCTGTAAATGTTCAATGCTTACACAAATAC 874
Db 789 aactgatlctctcttcagcattgtcttcgttaatgttcatgtctacacaacaatac 848
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Job time: 4307 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 1, 2002, 21:04:38 : Search time 92.08 Seconds
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Title: US-08-305-518-7

Perfect score: 1610
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 351203 seqs, 113238999 residues

Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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ALIGNMENTS

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RESULT 1
US-08-889-108-7
: Sequence 7, Application US/08889108
: Patent No. 6103492
: GENERAL INFORMATION:
: APPLICANT: Yu, Lei
: TITLE OF INVENTION: Mu Opioid Receptors: Compositions and Methods
: NUMBER OF SEQUENCES: 17
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Arnold, White & Durkee
: STREET: P. O. Box 4433
: CITY: Houston
: STATE: TX
: COUNTRY: USA
: ZIP: 77210-4433
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/889,108
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/305,518
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Wilson, Mark B.
: REGISTRATION NUMBER: 37,259
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 512-418-3000
: TELEFAX: 512-474-7577
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1610 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: US-08-889-108-7

Query Match 100.0%; Score 1610; DB 3; Length 1610;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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TOPOLOGY: linear
MOLECULE TYPE: CDNA
PCT-US94-10358-7

Query Match 100.0% Score 1610; DB 5; Length 1610;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
US-08-188-275A-1
Sequence 1, Application US/08188275A
Patent No. 6258556
GENERAL INFORMATION:
APPLICANT: Uhl, George R.
APPLICANT: Wang, Jia-Bei
APPLICANT: Johnson, Peter S.
APPLICANT: Persico, Antonio
TITLE OF INVENTION: CDNA and Genomic Clones Encoding Human
TITLE OF INVENTION: Mu Opiate Receptor and the Purified Gene Product
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22040-3487
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188, 275A
FILING DATE: 28-JAN-1994
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
 NAME: Murphy Jr., Gerald M.
 REGISTRATION NUMBER: 28,977
 REFERENCE/DOCKET NUMBER: 1173-449P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-241-1300
 TELEFAX: 703-241-2848
 TELEX: 248345
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2160 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: -
 LOCATION: 1..2160 /label= cDNA
 OTHER INFORMATION: /note= "cDNA encoding human mu opiate receptor"
 US-08-188-275A-1

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 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1567; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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RESULT 4
 US-08-889-108-1
 Sequence 1, Application US/08889108
 Patent No. 6103492
 GENERAL INFORMATION:
 APPLICANT: Yu, Lei
 TITLE OF INVENTION: Mu Opioid Receptors: Compositions and Methods
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold, White & Durkee

STREET: P. O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/889,108
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/305,518
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: INDA005\WIM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1618 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (cDNA)
FEATURE:
NAME/KEY: CDS
LOCATION: 214..1410
US-08-889-108-1

Query Match 69.8%; Score 1123.8; DB 3; Length 1618;
Best Local Similarity 83.7%; Pred. No. 3e-290;
Matches 1323; Conservative 0; Mismatches 247; Indels 11; Gaps 4;

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DB 295 TCTGTGCTCACTTGTCCACTTATGATGCAACCTGTCCGACCCATGCGGTCCGAACCGC 354
QY 386 ACCGAGCTGGGCGGAGAGACGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 445
DB 355 ACCGAGCTGGGCGGAGAGACGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 414
QY 446 GCCATCAGATCATGGCCCTTACTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 505
DB 415 GCATTAACCATCATGGCCCTTACTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 474

QY 506 CTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 565
DB 475 CTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 534
QY 566 TTCAACCTTGTCTGCGCAGATGCTTACGACGAGTACCTGCTTCCAGATGTGAT 625
DB 535 TTCAACCTTGTCTGCGCAGATGCTTACGACGAGTACCTGCTTCCAGATGTGAT 594
QY 626 TACTATAGGAGACATGGCCATTTGGACCATCTTGGACGATGATGATGATGATGATGATGAT 685
DB 595 TACTATAGGAGACATGGCCATTTGGACCATCTTGGACGATGATGATGATGATGATGATGAT 654
QY 686 TACTATAGGAGACATGGCCATTTGGACCATCTTGGACGATGATGATGATGATGATGATGAT 745
DB 655 TACTATAGGAGACATGGCCATTTGGACCATCTTGGACGATGATGATGATGATGATGATGAT 714
QY 746 GCAGTCTGCCACCTGTCAAGGCTTATGATTTCCGACTGCCGAAATGCAAAATATATC 805
DB 715 GCTGTGCGCCACGAGTCAAAAGCCCTGATTCGTAACCCCGCAAAATGCGTC 774
QY 806 AATGTGCGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 865
DB 775 AATGTGCGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 834
QY 866 ACAAAATACAGGAGGATTCATAGATTTGATACATTAATCTCTCATCAGACCTGATC 925
DB 835 ACAAAATACAGGAGGATTCATAGATTTGATACATTAATCTCTCATCAGACCTGATC 894
QY 926 TGGGAAACCTGCTGAGATCTGTGTTTCATCTTGCCCTTCAATATGCCAGTCTCATC 985
DB 895 TGGGAAACCTGCTGAGATCTGTGTTTCATCTTGCCCTTCAATATGCCAGTCTCATC 954
QY 986 ATTACGCTGCTATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1045
DB 955 ATTACGCTGCTATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1014
QY 1046 TCCAAAGAAAGAGACAGAAATCTTCAGAGATCACCAGATGCTGCTGCTGCTGCTGCTGCTGCT 1105
DB 1015 TCCAAAGAAAGAGACAGAAATCTTCAGAGATCACCAGATGCTGCTGCTGCTGCTGCTGCTGCT 1074
QY 1106 GTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1165
DB 1075 GTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1134
QY 1166 ATCCGAAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1225
DB 1135 ATCCGAAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1194
QY 1226 AACAGCTGCTCAACCACTCTTATGCAATTTCTGATGAAACCTTCAAAACGATGCTTC 1285
DB 1195 AACAGCTGCTCAACCACTCTTATGCAATTTCTGATGAAACCTTCAAAACGATGCTTC 1254
QY 1286 AGAGCTTCTGATTCACCACTCTTCAACATTTGACCAACAAACCTCACTCAATTCCT 1345
DB 1255 AGAGCTTCTGATTCACCACTCTTCAACATTTGACCAACAAACCTCACTCAATTCCT 1314
QY 1346 CAGAACCTAGAGACACCTCTCAGAGCAGCAATAGAGTGAATCAATCAATCAATCAATCAATCAAT 1405
DB 1315 CAGAACCTAGAGACACCTCTCAGAGCAGCAATAGAGTGAATCAATCAATCAATCAATCAATCAAT 1374
QY 1406 GAAATCTGAGAGCAAAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1465
DB 1375 GAAATCTGAGAGCAAAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1434
QY 1466 TCACCAAGCTTGAAGCAGCAACCATGATGAGGAGGTTGCTTCAAGATGATGATGATGATGATGATGAT 1525
DB 1435 TCACCAAGCTTGAAGCAGCAACCATGATGAGGAGGTTGCTTCAAGATGATGATGATGATGATGATGAT 1494
QY 1526 GCTTAATCTCTAGAGAAAGTGTCTGCTTATGATATCAACCTCTTCTGCTGCTGCTGCTGCTGCTGCT 1585
DB 1495 GCTTAATCTCTAGAGAAAGTGTCTGCTTATGATATCAACCTCTTCTGCTGCTGCTGCTGCTGCTGCT 1551
QY 1586 ACTTGTCTGACATTTAGAG 1606

Db 1552 ACTTCACCTCTGCACATGAGAG 1572
|||||
RESULT 5
US-08-889-108-3
Sequence 3, Application US/08889108
Patent No. 6103492
GENERAL INFORMATION:
APPLICANT: Yu, Lei
TITLE OF INVENTION: Mu Opioid Receptors: Compositions and Methods
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/889,108
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/305,518
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: INDA005\WIM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-5000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1618 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (cDNA)
FEATURE:
NAME/KEY: CDS
LOCATION: 339..1235
US-08-889-108-3
Query Match 69.8%; Score 1123.8; DB 3; Length 1618;
Best Local Similarity 83.7%; Pred. No. 3e-290;
Matches 132; Conservative 0; Mismatches 247; Indels 11; Gaps 4;

Db 241 ACCAGCAGCTGCTCAGACCCCTTAGCTCAGGCAAGTTGCTCCACGCA-----CTGGC 294
Qy 326 TCCTGGGCTCAACTTGTCCCACTTAGATGGCAACCTGTCCGACCAGCTGGTCCGAACCG 385
Db 295 TCCTGGGCTCAACTTGTCCCACTTAGATGGCAACCTGTCCGACCAGCTGGTCCGAACCG 354
Qy 386 ACCGACCTGGGCGGAGAGACAGCTGTGCTCCGACCGGCAAGTCCCTCATGATCAG 445
Db 355 ACCGGCTGGGCGGAGAGACAGCTGTGCTCCGACCGGCAAGTCCCTCATGATCAG 414
Qy 446 GCCATACAGTCAATGAGCCCTACTCATGCTGTGCTGGTGGGCTTCCGAACCTTC 505
Db 415 GCCATTACCATGAGCCCTACTCATGCTGTGCTGGTGGGCTTCCGAACCTTC 474
Qy 506 CTGCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 565
Db 475 CTGCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 534
Qy 566 TTCAACCTTGTCTGGCAGATGCTTACCCACAGTACCTGCTTCCAGAGTGTGAT 625
Db 535 TTCAACCTTGTCTGGCAGATGCTTACCCACAGTACCTGCTTCCAGAGTGTGAT 594
Qy 626 TACCTAATGGGAACATGGCCATTTGGAAACATCCTTTGCAAGATAGATCTCATGAT 685
Db 595 TACCTAATGGGAACATGGCCATTTGGAAACATCCTTTGCAAGATAGATCTCATGAT 654
Qy 686 TACTATACATGTTTACACAGCATATTCACCTCTGCACATGATGTTGATGATCAT 745
Db 655 TACTATACATGTTTACACAGCATATTCACCTCTGCACATGATGTTGATGATCAT 714
Qy 746 GCACTGTGCCACCTGTGCAAGGCTTAGATTCCGTACTCCGGAATGCAAAATATC 805
Db 715 GCTGTGTGCCACCTGTGCAAGGCTTAGATTCCGTACTCCGGAATGCAAAATC 774
Qy 806 AATGTGTGCAACTGGATGCTCTCTGACGATGTTGTTGTTGTTGTTGTTGTTGTTG 865
Db 775 AATGTGTGCAACTGGATGCTCTCTGACGATGTTGTTGTTGTTGTTGTTGTTGTTG 834
Qy 866 ACAAAATACAGGCAAGTTCATAGATTGTACATACTCTCTCTCTCTCTCTCTCTCT 925
Db 835 ACAAAATACAGGCAAGTTCATAGATTGTACATACTCTCTCTCTCTCTCTCTCTCT 894
Qy 926 TGGGAAACCTGCTGAAGATCTGTTTTCATCTTGCCTTCATTTAGCCAGTGTATC 985
Db 895 TGGGAAACCTGCTGAAGATCTGTTTTCATCTTGCCTTCATTTAGCCAGTGTATC 954
Qy 986 ATTACGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1045
Db 955 ATTACGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1014
Qy 1046 TCCAAAGAAAGACAGGATCTTTCGAAGATACACAGATGCTGCTGCTGCTGCTGCT 1105
Db 1015 TCCAAAGAAAGACAGGATCTTTCGAAGATACACAGATGCTGCTGCTGCTGCTGCT 1074
Qy 1106 GTGTTTATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1165
Db 1075 GTATTTATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1134
Qy 1166 ATCCAGAAACCTGCTGCAAGATGTTTGGACATCTGCAATGCTGATGATGATG 1225
Db 1135 ATCCAGAAACCTGCTGCAAGATGTTTGGACATCTGCAATGCTGATGATGATG 1194
Qy 1226 AACAGCTGCTTCAACCCAGTCTTATGATGATGATGATGATGATGATGATGATGAT 1285
Db 1195 AACAGCTGCTTCAACCCAGTCTTATGATGATGATGATGATGATGATGATGATGAT 1254
Qy 1286 AGAGATGTTGATATCCCACTCTTCCACATGATGATGATGATGATGATGATGAT 1345
Db 1255 AGAGATGTTGATATCCCACTCTTCCACATGATGATGATGATGATGATGATGAT 1314
Qy 1346 CAGAACATAGAGACACCCCTCCAGGCAATACAGTATGATGATGATGATGATGAT 1405
Db 1315 CAGAACATAGAGACACCCCTCCAGGCAATACAGTATGATGATGATGATGATGATG 1374

Oy	1226	AACGAGGCCCAACCCAGACGCTTTTANGATTTCTGGATGAACCTTCAAGGATGCTC	1285
Db	1195	AACGAGCTGCCGAATCCAGTTCTTTTAAGCCTTCTTGATGAACCTTCAAGGATGCTTC	1254
Oy	1286	AGAGAGTTCTGTATCCCAACCTCTTCCAACTTGGACCAACAAACCTCCACTGGAATTCGT	1345
Db	1255	AGAGAGTTCTGCATCCCAACCTCTGTCCAGATGGAACAGCAAAACCTCCACTGGAATTCGT	1314
Oy	1346	CAGAACACTAGAGACCACCCCTCCACGGCCATATACGTGGATAGAACTATATCATGCTA	1405
Db	1315	CAGAACACTAGGGAAACATCCCTCCACGGCTAAATACAGTGATCGAACTAACACACAGCTA	1374
Oy	1406	GAAATCTGGAGAGCAAAACCTGCTCGGTGGCCCTAACAGGGTCTATCGCAATCCGACT	1465
Db	1375	GAAATCTGGAGGCAAGAACTGCTCCATTTGCCCTTAATCTGGTCTCACACATCCAGACCC	1434
Oy	1466	TCACCAAGCTTAGAAGCCACCATGTATGTGGAAAGCAGGTTGCTCAAGATGTGTAGAG	1525
Db	1435	TCGCTAAATCTTAGAGGCGCGGCACATCTACGTGGAACTACAGTTGCTGTACGGGTGTGTGGAG	1424
Oy	1566	GCTCTAATCTCTAGAGAAAGTGCCCTCTTTAAGTCATCAACCTCTTTCTCTGTGGCC	1585
Db	1495	GCTCTGGTTTCTTCAGAAA---CCATCTGATCTCGATTCAAAGATCATCTCTGTGCT	1551
Oy	1586	ACTCTGCTGCACATATAGAG	1606
Db	1552	ACTTCACCTGCACATGAG	1572

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RESULT 7
US-08-120-601B-3
Sequence 3, Application US/08120601B
Patent No. 6235496
GENERAL INFORMATION:
APPLICANT: Yu, Lei
TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/120,601B
FILING DATE: 13-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: INDA:002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1618 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 339..1232
US-08-120-601B-3

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Query Match	69.8%;	Score 1123.8;	DB 4;	Length 1618;
Best Local Similarity	83.7%;	Pred. No. 3e-290;		
Matches 1323;	Conservative 0;	Mismatches 247;	Indels 11;	Gaps 4;

OY	27	GTGGGAGGGGGCTTACGAGAGAGAAATTCAGATGCTCAGCTGGTCCCTCGCCCTG	86
Db	2	GTGGAGGGGGCTCAAGCAGAGAGAGAAATTCAGACGCTCAGA - GCTTCCTCTTGCCCTG	60
OY	87	ACGCTCCTCTCTGTCTCAGCCAGGACTGGTTTCTGTAAAGAACAGCAGAG - CTGTGGCA	145
Db	61	CCGGCTCTTCTTGTTTCCACTATAGGGCTGTCATGTAAAAATCTGACAGGGCTAGGGCA	120
OY	146	GGCGGAGAAAGGAACGGCTCAGGCGGCTGTGAACCCGAAAGTCTGGTGTCTCTAGCTAC	205
Db	121	GCTGTGAGAGAGAGAGAGGCTTGGGGCGCTGSGAACCCAAAAGTCTGAGTCTTCAGATTAC	180
OY	206	CTCGCAGAGCGTGGCCCGCCGGCCGTCAGTACATGAGCAGAGCGGTGCCCCAGAAC	265
Db	181	AGGCTACCTATGTCCGACGAGGCGCTTCAGACCATGAGCAGCAGCACGGGCCAGGAAAC	240
OY	266	GGCAGCAATTGTCACTGATGECTTGGGGTACTCAAGTTGCTCCCCAGACACCCAGCCCGGT	325
Db	241	ACCGAGCGAGCTGTGAGACCCCTTAGCTCAGGCAAGTGGTCTCCACACA - - - - - CTTGGC	294
OY	326	TCCGCGGCTCAACTGTGCCACTTAGATAGTGAACCTCTCGACCATCGGCTCCGAGAACGC	385
Db	295	TCTGTGGCTCAACTTGTGCCACGTTTGATGAGAACCAATCCGATTCAGTGGGCTTGAAACGC	354
OY	386	ACCGACCTGGGGGGAGAGAGACGCTGTGGCCCTCGGACCGGAGTCCCTCATGTATCAG	445
Db	355	ACCGGGGCTTGGCGGGAACGACACGCTGTGCCCTCAACACCGGACGCGCTTCATGTGTACA	414
OY	446	GGCATACAGATCAGGGCCCTCTACTCATGTGTGGTGTGGGGGCTCTTGAGAAATTC	505
Db	415	GCCATTACCATATGCGCCCTCTACTCTATCGTGTGTGTGTGTGGGCTCTTGGGAAATTC	474
OY	506	CTGGTCACTGATGTGATTTGTCAGATACACCAAGATGAAGACTGCCACCAATCTACATT	565
Db	475	CTGGCATGATGTGATTTGATTTGAATGATACACAAATGAAGACTGCCACCAATCTACATT	534
OY	566	TTTCAACTTGTCTCTGGCAGATGCCCTTAGCCACAGTACCTCGCTTCCAGAGTGTGAT	625
Db	535	TTTCAACTTGTCTCTGGCAGAGCGCTTAGGACACAGTACCTGCCCTTTCAGATGTCTACAC	594
OY	626	TACCTAATGGGAACATGATGCCATTGTGGACCATCTTTGGAAGTATGATGTCCATATAT	685
Db	595	TACCTGATGGGAACATGATGCCCTTGGGAACCATCTCTTGAAGATGTGATGTCCATATAT	654
OY	686	TACTATACATGTTCAACAGCATATTACCCCTCTGCACCATGAGTTGATGATACATT	745
Db	655	TACTATACATGTTCAACAGCATATTACCCCTCTGCACCATGAGTGTGACCGTACATT	714
OY	746	GCACTCGCAACCTGTGCAAGGGCTTAAGTTTCCGATCCCGCGAAGTCCGCAAAATTTATC	805
Db	715	GCTGTGCGCAACCGAGTCAAGCCCTGTGATTCGATCCGACCCCGGAAATGCAAAATTCGTC	774
OY	806	AATGTGTGCACTGTGATCCCTCTTAGAGCATGTGCTTCTCGTATGTTTCATGTGCTACA	865
Db	775	AAGTGTGTGCAACTGTGATCCCTCTTCTGCGATGGGTGCTGCTGATGTTCATGTGCAACCC	834
OY	866	ACAAATAATACAGGCAAGGTTTCATAGATTGTACACTAACATTCTTCATATCCAACTGTGTAC	925
Db	835	ACAAATAATACAGGCAAGGGGTTCATAGATTGACACCTTCACCTTCCACCAACTGTGTAC	894
OY	926	TGGGAAGAACCGGCGAAGATCTGTGTTTTCATCTTGCCCTTCATTATGGCAGTGGCTATC	985
Db	895	TGGGAAGAACCTGCTCAAAATCTGTCTTATCTTCTGCTTTCATATGCGCATCTCTATAC	954
OY	986	ATTACCGCTGTGCTATGTGACTGATGATCTTGGGCTTCAAAATGTCCGAGTGCCTCTAGC	1045
Db	955	ATCACGTGTGTGTACGGCGTATGATCTTACAGACTAAAGAGGTTTGCATGTGTATACGGGC	1014
OY	1046	TCCAAAGAAAAGCAGGAATCTTTCGAGAGATCCACGAGATGTGCTGTGTGTGCT	1105

||||| 1015 TCCAAAGAAAGACAGGATCTGGCCAGATCCACCCGATGCTGTGGTCGGCT 1074
QY 1106 GTGTTATGCTGCTGAGACTGCTCATTTACATTTAGCATTTAAACCTTGGTTAC 1165
Db 1075 GTATTATATGCTGCTGGAGCCCATTCACATCTAGCTATCATCAAGCGCTGATCAG 1134
QY 1166 ATCCAGAAACTAGTTCAGACTGTTCTTGGCACTTCGATTCGCTAGTTACACA 1225
Db 1135 ATTCAGAAACCATTTACAGACGTTTCTGCACTTCGATTCCTTTGGGTTACAG 1194
QY 1226 AACAGTGCCTAACCCATCTTTATGATTTTGTGATGAAAACTTCAAAGCTTTC 1285
Db 1195 AACAGTGCCTAACCTTCTTACGCTTCGATGAAAACTTCAAAGGATGCTTC 1254
QY 1286 AGAGATTCGTATCCCACTCTTCCAACTTGGACAAACAACTCCGATTCG 1345
Db 1255 AGGATTCGTATCCCACTCTTCCAACTTGGACAAACAACTCCGATTCG 1314
QY 1346 CAGAACTAGAGACACCCCTCCAGGCAATACAGTGAATAGAACTATCATCAGTA 1405
Db 1315 CAGAACTAGAGACACCCCTCCAGGCAATACAGTGAATAGAACTATCATCAGTA 1374
QY 1406 GAAATCTGGAAGCAAACTGCTGCTGCTTCCCTAACAGGCTCTCATTCGACCT 1465
Db 1375 GAAATCTGGAAGCAAACTGCTGCTGCTTCCCTAACAGGCTCTCATTCGACCT 1434
QY 1466 TACCAAGCTTGAAGCCCACTGATGTGGAAGAGGTTGCTTCAAGATGTGAGAG 1525
Db 1435 TCGCTAGCTTGAAGCCCACTGATGTGGAAGAGGTTGCTTCAAGATGTGAGAG 1494
QY 1526 GCTCTAATCTCTAGAAAGTGCTGCTTTTAGTGATCCAACTCTTCTCTGAGCC 1585
Db 1495 GCTCTAATCTCTAGAAAGTGCTGCTTTTAGTGATCCAACTCTTCTCTGAGCC 1551
QY 1586 ACCTGCTCTGCACATTAAG 1606
Db 1552 ACTTACTCTGCACATGAAG 1572

RESULT 8
PCT-US94-10358-1
Sequence 1, Application PC/TUS9410358
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10358
FILING DATE: Concurrently herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/120,601
FILING DATE: 13 SEPTEMBER 1993
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARK B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: INDIA005P--
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679

TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1618 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 214..1410
; PCT-US94-10358-1

Query Match 69.8%; Score 1123.8; DB 5; Length 1618;
Best Local Similarity 83.7%; Pred No. 3e-290;
Matches 1323; Conservative 0; Mismatches 247; Indels 11; Gaps 4;

QY 27 GTGGAGAGGGGCTATACGAGAGAGAAATGTGAGATGCTGACCTGGTCCCTCCGCTG 86
Db 2 GTGGAGAGGGGCTATACGAGAGAGAAATGTGAGATGCTGACCTGGTCCCTCCGCTG 60
QY 87 AGGCTCTCTCTGTCTGACAGCAGAGACTGTTCTGTAAAGAAACAGCAGAG-CTGTGGA 145
Db 61 CGGCTCTCTGTGTGTTGCTGACTAGAGGCTGTCCATGTAAAGAAATCTAGAGGCTAGGGA 120
QY 146 GCGGCGAAAGAGAGCGGCTGAGAGCGCTTGGAAACCGAAAGTCTGCTGCTCCGCTAC 205
Db 121 GCTGTGAGAGAAAGAGGCTGGGGCGGTGGAACCGAAAGTCTGAGTCTCTCAGTTAC 180
QY 206 CTGCGACAGCGTCCCGCGCGGCGCTGACCTACATGAGCAGCAGCGCTGCCCCAGAAC 265
Db 181 AGCTTACCTAGTACCGGAGAGGCGCTTACACCATGAGCAGCAGCAGCGCGCCAGGAAAC 240
QY 266 GCGAGCAATTTGACATGATGCTTGGGCTGCTCAAGTTGCTCCGACGACCGACCCGGT 325
Db 241 ACCAGGACTGCTCAGACCCCTTAGCTCAGGCAAGTTGCTCCGACGACGACGACGACG 294
QY 326 TCGTGGTCACTTGTCCCACTTATGATGCAACCTGTCCGACCATGCGGTCCGAACCGC 385
Db 295 TCGTGGTCACTTGTCCCACTTATGATGCAACCGGTGATGCAACCGGTGCTGGAACCGC 354
QY 386 ACCGACCTGGGCGGAGAGACAGCTGTCCCTCCGACCGCAGTCCCTCATGTATCAGC 445
Db 355 ACCGACCTGGGCGGAGAGACAGCTGTCCCTCCGACCGCAGTCCCTCATGTATCAGC 414
QY 446 GGCATCAGATATGCGCCCTTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 505
Db 415 GGCATCAGATATGCGCCCTTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 474
QY 506 CTGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 565
Db 475 CTGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 534
QY 566 TTCAACCTTGTCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 625
Db 535 TTCAACCTTGTCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 594
QY 626 TACCTAATGGAACATGCGCATTTGGAACATGCTTGGCAATGATGATGATGATGATGATG 685
Db 595 TACCTAATGGAACATGCGCATTTGGAACATGCTTGGCAATGATGATGATGATGATGATG 654
QY 686 TACTATACATGTTACACGACATATTCACCTCTGACCATGAGTGTGATGATGATGATGAT 745
Db 655 TACTATACATGTTACACGACATATTCACCTCTGACCATGAGTGTGATGATGATGATGAT 714
QY 746 GCACTGCGACCTGTGCAAGGCTTATGATTCGCTACTCCCGAAATGCCAAATATATC 805
Db 715 GCTGCTGCGACCTGTGCAAGGCTTATGATTCGCTACTCCCGAAATGCCAAATATATC 774
QY 806 AATGCTGCAAGTGAATCTCTCTTCAAGCATTTGATGCTTCTGATGATGATGATGATGAT 865
Db 775 AATGCTGCAAGTGAATCTCTCTTCAAGCATTTGATGCTTCTGATGATGATGATGATGAT 834

OY	886	ACAAAATACAGGCAAGGCTTCATAGATTGACACTAAATCTCATATCAACCTGATAC	925
Db	885	ACAAAATACAGGCAAGGCTTCATAGATTGACACTAAATCTCATATCAACCTGATAC	894
OY	926	TGGGAAAACCTGCTGAAGATCTGTGTTTCATCTTGCCCTTATATGCAAGTCTCATC	985
Db	895	TGGGGAACCTGCTCAAAAATCTGTGTTTCATCTTGCCCTTATATGCAAGTCTCATC	954
OY	986	ATTACCGTGCTGTGACACGTAGATGATCTTGCGCTCAAGAGTGCTCGAATGCTCTGAC	1045
Db	955	ATCACGTGTGTTTACGCGCTGATGATCTTACGACTCAAGAGGCTTGCAATGCTATCGGCG	1014
OY	1046	TCCAAGAAAAAGCAGAGAACTCTTCGAAGAGTACCAGAGATGGTGTGCTGATGCT	1105
Db	1015	TCCAAGAAAAAGCAGAGAACTCTTCGCGAGAGATCACCGGATGGTGTGCTGATGCT	1074
OY	1106	GTTGTTACGTCTGCTGAGACTCCCATTTACATTTACGTATCATTTAAGCCTTGTTACA	1165
Db	1075	GTAATTATTCGTCTGCTGAGCCCCCATTCACATTTAGTCATCATCAACGCTGATACAG	1134
OY	1166	ATCCAGAAAATAGGTTCCAGAGCTGTTCTTGCGACTCTTGCGATTCGCTAGTATACACA	1225
Db	1135	ATTCAGAAAACCATATTTCAAGCCGTTCTTGCGACTTTCGATGCTTGTGGTTACAG	1194
OY	1226	AACAGTCCCTCAACCCAGTCTTTATGCAATTTCTGGATGAAAACTTCAACGATGCTTC	1285
Db	1195	AACAGTCCCTCAAGTTCAGTTCCTTTACGCTTCTGATGATGAAAACTTCAAGGATGCTTC	1254
OY	1286	AGAGAGTTCTGTATTCACACCTCTTCCACATTTAGACACAAAACTCCACTGGAATTGCT	1345
Db	1255	AGAGAGTTCTGTCAATCCCAACCTGCTCCACGATGGAACAGAAAACTCCACTGAGTCCGT	1314
OY	1346	CAGAACTAGAGACCAACCCCTCCAGGGCCAAATACAGTGGAATGAACTAATCATAGCTA	1405
Db	1315	CAGAACTAGAGGAACATCTCCTCAGCGCTAATATACAGTGATGACATACCAACGACTA	1374
OY	1406	GAATAATCTGAAGCAGAAACTGCTCCGTTTGCCCTTAACAGGGTCTCATGCCATTCGAGCT	1465
Db	1375	GAATAATCTGAGGCAGAAACTGCTCCATTCCTTACTGGGTCTACACCATTCAGAACCC	1434
OY	1466	TCACCAAGCTTAGAAGCCACCATGTATGTGGAAGAGGTTGCTTCAAGAAATGTATAGAG	1525
Db	1435	TCGCTAACCTTAGAGGCCCATCTATCTAGCTGAATCAGGTTGCTGTCAAGGTTGTGGAG	1494
OY	1526	GCTCTAATCTCTAGAAAGGCTGCTTTTAGATGATCAATCAACCTCTTCTCTGAGCC	1585
Db	1495	GCTCTGTTTCTCTAGAAA---CCATGTATCTCTGATTCAAAGTCAATTCCTCTGCT	1554
OY	1586	ACTCTGCTCTGCACATTAGAG 1606	
Db	1552	ACTCTACTCTGCACATAGAG 1572	
RESULT	9		
	PCT-US94-10358-3		
	Sequence 3, Application PC/TUS9410358		
	GENERAL INFORMATION:		
	APPLICANT:		
	TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS		
	NUMBER OF SEQUENCES: 17		
	CORRESPONDENCE ADDRESS:		
	ADDRESSEE: Arnold, White & Durkee		
	STREET: P. O. Box 4433		
	CITY: Houston		
	STATE: Texas		
	COUNTRY: USA		
	ZIP: 77210		
	COMPUTER READABLE FORM:		
	MEDIUM TYPE: Floppy disk		
	COMPUTER: IBM PC compatible		
	OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII		
	SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25		

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Db 595 TACCGATGGGAACATGGCCCTTGGAAACATCCCTCAGATGTGATCTCAATTAAT 654
Oy 686 TACTTAACATGTTTACAGACATATTCACCTCTGACACATGAGTGTGATGATACAT 745
Db 655 TACTTAACATGTTTACAGACATATTCACCTCTGACACATGAGTGTGATGATACAT 714
Oy 746 GCAGTCTGCCACCCGTGCAAGGCTTGTAGATTTCCGTACTCCCGAATATTC 805
Db 715 GCTGTCTGCCACCCGTGCAAGGCTTGTAGATTTCCGTACTCCCGAATATTC 774
Oy 806 AATGCTCTGCAACTGATATCTCTCTTACACCATTTGTTCTCTGTAATGTTCATG 865
Db 775 AACGCTCTGCAACTGATATCTCTCTTCTTCTGCAACGCTGCTGTAATGTTCATG 834
Oy 866 ACAAAATACAGGACAGGAGGTTCATATGATGATGATGATGATGATGATGATGAT 925
Db 835 ACAAAATACAGGACAGGAGGTTCATATGATGATGATGATGATGATGATGATGAT 894
Oy 926 TGGGAAACCTGCTGAGATGATGATGATGATGATGATGATGATGATGATGATG 985
Db 895 TGGGAAACCTGCTGAGATGATGATGATGATGATGATGATGATGATGATGATG 954
Oy 986 ATTACCGTGTCTATGATGATGATGATGATGATGATGATGATGATGATGATG 1045
Db 955 ATCTGCTGTGTGTAGGCTGATGATGATGATGATGATGATGATGATGATGATG 1014
Oy 1046 TCCAAAGAAAGGACAGGATGATGATGATGATGATGATGATGATGATGATGAT 1105
Db 1015 TCCAAAGAAAGGACAGGATGATGATGATGATGATGATGATGATGATGATGAT 1074
Oy 1106 GTGTTTATGCTGTGCTGATGATGATGATGATGATGATGATGATGATGATG 1165
Db 1075 GTATTTATGCTGTGCTGATGATGATGATGATGATGATGATGATGATGATG 1134
Oy 1166 ATCCGAGAACTAGCTTCCAGACTGTTTCTGAGCTTCTGATGATGATGATGAT 1225
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Oy 1226 AACAGCTGCTGCAACCCGCTGCTGATGATGATGATGATGATGATGATGATG 1285
Db 1195 AACAGCTGCTGCAACCCGCTGCTGATGATGATGATGATGATGATGATGATG 1254
Oy 1286 AGAGATGCTGTATGCAACCTCTTCAACATGAGCAACAACTGCACTGATGCT 1345
Db 1255 AGAGATGCTGTATGCAACCTCTTCAACATGAGCAACAACTGCACTGATGCT 1314
Oy 1346 CAGAACACTAGAGACACCCCTCCAGGCGCAATACAGTGTGATGATGATGAT 1405
Db 1315 CAGAACACTAGAGACACCCCTCCAGGCTAATACAGTGTGATGATGATGATG 1374
Oy 1406 GAAATCTGGAAGCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1465
Db 1375 GAAATCTGGAAGCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1434
Oy 1466 TCACCAAGCTTAGAAGCACCATGATGTGGAAGCAGGTGCTGCTGCTGCTG 1525
Db 1435 TCACCAAGCTTAGAAGCACCATGATGTGGAAGCAGGTGCTGCTGCTGCTG 1494
Oy 1526 GCTCTAATTTCTAGGAAAGTGTCTTTAGTGTATGATGATGATGATGATG 1585
Db 1495 GCTCTAATTTCTAGGAAAGTGTCTTTAGTGTATGATGATGATGATGATG 1551
Oy 1586 ACTGCTGCTGACATTTAG 1606
Db 1552 ACTTCACTCTGACATGAGAG 1572

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RESULT 10
 US-08-387-707-15
 : Sequence 15, Application US/08387707
 : Patent No. 6265563
 : GENERAL INFORMATION:

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: APPLICANT: EVANS, CHRISTOPHER J.
: APPLICANT: KEITH, DUANE E.
: TITLE OF INVENTION: OPIOID RECEPTOR GENES
: NUMBER OF SEQUENCES: 18
: CORRESPONDENCE ADDRESS:
: ADDRESS: MORRISON & FOERSTER
: STREET: 2000 Pennsylvania Avenue, N.W. Suite 5500
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20006-1888
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/387,707
: FILING DATE: 10-SEP-1995
: CLASSIFICATION: 536
: ATTORNEY/AGENT INFORMATION:
: NAME: MURASHIGE, KATE H.
: REGISTRATION NUMBER: 29,959
: REFERENCE/DOCKET NUMBER: 22000-20526, 20
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 887-1500
: TELEFAX: (202) 887-0763
: INFORMATION FOR SEQ ID NO: 15:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1981 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: US-08-387-707-15

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Query Match 69.2%, Score 1114.6, DB 4, Length 1981:
Best Local Similarity 83.1%, Pred. No. 9.2e-288:
Matches 1319; Conservative 0; Mismatches 260; Indels 9; Gaps 4:

Oy 4 ATGAGCCTCTGTGACTACTAGTGTGGAGGGGCTATTACGAGAGGAATGTCAGATG 63
Db 20 AAGCCCTCTCGTACTCTTAAAGTGGAGGGGATACAGAGAGGAATATGAGACG 79
Oy 64 CTGACCTGGTCCCTCCGCTGAGCTCTCTCTGTCAGCCAGACTGTTTCTGTA 123
Db 80 CTCAC-ACGTTTCATTTGCTGCGCGCTCTCTCTGTTCCACTAGGGCTGTCTTGA 138
Oy 124 AGAAGACGAGAG-CTGTGACAGCGCGGAAAGAGAGCGCTGAGGCGCTTGAACCGA 182
Db 139 AGAAGACGAGAGCGCTGAGGCGAGTGTAGAGAGAGAGGCGCGCTTGAACCGGA 198
Oy 183 AAGTCTGG-GTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 241
Db 199 ACATCTTGTAGTGTCTGATGATGATGATGATGATGATGATGATGATGATGATG 258
Oy 242 GACAGCAGCGCTGCCCCAGCAGCAATGCACTGATGCTTGGCTTACTCAAGT 301
Db 259 GACAGCAGCGCGCGCCAGAGGAATCAAGCAGCTCTGACACCCCTTATGCTTCAAGT 318
Oy 302 TGCTCCCGAGCAGCCCGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 361
Db 319 TGCTCCCGAGCA-----CTTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 372
Oy 362 TCCGAGCCATGGGTCGCAACCGCAGCAGCGGCGGAGAGAGAGCGCTGCGCTCG 421
Db 373 TCCGAGCCATGGGTCGCAACCGCAGCAGCGGCGGAGAGAGAGCGCTGCGCTCG 432
Oy 422 ACCGCGAGTCCCTCCATGATACAGGCGCATCAGATGATGATGATGATGATGATG 481
Db 433 ACCGCGAGCGCTTCCATGATGATGATGATGATGATGATGATGATGATGATGATG 492
Oy 482 GTGTGGGGCTCTTGGAACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 541

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Db 493 GTAGTGGGCTCTTTGAAACTTCGTGTCATGTATGTATGATATACCAATG 552
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Db 553 AAGATGGCCCAACATCTCATTTTCAACCTGCTGTGGCAATGCTTACGACAGT 612
OY 602 ACCCTGCCCCCTCCAGATGTAATTCATATGGAACATGAGCATTTGGACATCTCT 661
Db 613 AGCTTCCCTTTTACAGATGTAATTCATATGGAACATGAGCATTTGGACATCTCT 672
OY 662 TGCAGATAGTATGATCTCATATGATATGATATGATATGATATGATATGATAT 721
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OY 722 ACCATGAGTGTATGATATGATATGATATGATATGATATGATATGATATGATAT 781
Db 733 ACCATGAGTGTATGATATGATATGATATGATATGATATGATATGATATGATAT 792
OY 782 ACTCCCGAATGCAAAATTTATCATGTCGACATGATCTCTCTCTCTCTCTCTCT 841
Db 793 ACCCGCGAATGCAAAATTTATCATGTCGACATGATCTCTCTCTCTCTCTCTCT 852
OY 842 CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 901
Db 853 CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 912
OY 902 ACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 961
Db 913 ACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 972
OY 962 GCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1021
Db 973 GCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1032
OY 1022 AAGATGTCGCGATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1081
Db 1033 AAGATGTCGCGATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1092
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OY 1142 GTCATCATTAAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1201
Db 1153 GTCATCATTAAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1212
OY 1202 TCTCTGATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1261
Db 1213 TCTCTGATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1272
OY 1262 GATGAAGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1321
Db 1273 GATGAAGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1332
OY 1322 CAACAAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1381
Db 1333 CAACAAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1392
OY 1382 GTGAGATAGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1441
Db 1393 GTGAGATAGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1452
OY 1442 CAGGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1501
Db 1453 CAGGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1512
OY 1502 GGTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1561
Db 1513 GGTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1572
OY 1562 ATCCAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1589

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Db 1573 ATCCAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1600

RESULT 11
US-08-430-286A-1
; Sequence 1, Application US/08430286A
; Patent No. 6225080
; GENERAL INFORMATION:
; APPLICANT: Enpl, George R.
; APPLICANT: Enpl, C. Mark
; APPLICANT: Wang, Jai-Bel
; TITLE OF INVENTION: Mu-Subtype Opioid Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: US
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,286A
; FILING DATE: 28-APR-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Robinson, Joseph R.
; REGISTRATION NUMBER: 33,448
; REFERENCE/DOCKET NUMBER: 0646/1A843-US5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2135 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; ORIGINAL SOURCE:
; ORGANISM: Rattus rattus
; IMMEDIATE SOURCE:
; CLONE: mu receptor cDNA
; US-08-430-286A-1

Query Match 64.1%; Score 1031.6; DB 4; Length 2135;
Best Local Similarity 84.7%; Pred. No. 1.3e-265;
Matches 1183; Conservative 0; Mismatches 204; Indels 9; Gaps 2;

OY 211 ACAGCGTCCCGCCGCGCGCTACATGACATGACAGCAGCGCTGCCCGACGAAAGCCAG 270
Db 3 ACTAGTCCGACAGACGCTTACGACATGACATGACAGCAGCGCGCGACGAAAGCCAG 62
OY 271 CAATTGCACTGATGCTTGGCGTACTCAAGTTCCTCCCGACGACCGCCGCTTCG 330
Db 63 CGACTCTCAGACCCCTTACGCTACGAGGAGTTCCTCCGACA-----CTGGGCTCTG 116
OY 331 GGCACACTTGTCCCACTTGTATGATGACCACTGTCCGACCGCATGCGAGTCCGACCGA 390
Db 117 GCTCAACTTGTCCCACTTGTATGATGACCACTGTCCGATGCGAGTCTCAACCGCACCG 176
OY 391 CCTGGCGGGAAGACAGCGCTGCGCTCGACCGGACAGTCCCTCCATGATCAGCGCAT 450
Db 177 GCTGGCGGGAAGACAGCGCTGCGCTCGACCGGACAGTCCCTCCATGATGATCAGCGCAT 236
OY 451 CAGATCATGCGCTCTACTCATGCTGTGCGTGGTGGGCTCTTGGAACTTCTCTGCT 510

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Db 237 TACCATCATGCCCCCTTACTATGTGTGTAGTGGCCCTCTTGGAACTCTCTGCT 296
 Oy 511 CATGTATGTATGTTCAGATACACCAAGATGAAGATGGCCACCAACATCTACATTTTCA 570
 Db 297 CATGTATGTATGTATGAATACACCAAAATGAAGATGGCCACCAACATCTACATTTTCA 356
 Oy 571 CCTTCTCTGGCAGATGGCTTAAGCCACAGTACCTGCCCTTCCAGAGTGTGATTAACCT 630
 Db 357 CCTTCTCTGGCAGAGCGCTTAGCCACAGTACACTGGCCCTTCCAGAGTGTGATTAACCT 416
 Oy 631 ATGGGACATGGCATGTGGAAACCATCTCTTGGCAAGATGGATCTCATATGATTACCA 690
 Db 417 GATGGGAAACATGGCCCTTGGAAACCATCTCTTGGCAAGATGGATCTCATATGATTACCA 476
 Oy 691 TAACATGTTCACACAGATATTCACCCCTGACACCATGATGTGTGATGATTAACCT 750
 Db 477 CAACATGTTCACACAGATATTCACCCCTGACACCATGATGTGTGATGATTAACCT 536
 Oy 751 CTGCCACCCCTGCAAGCCCTTAGATTTCCGTACCTCCCGAAATGCGAAATTAATGATGT 810
 Db 537 CTGCCACCCCTGCAAGCCCTTAGATTTCCGTACCTCCCGAAATGCGAAATTAATGATGT 596
 Oy 811 CTGCCACCTGATCTCTCTTCCGACATGTGTCTCTGTATGTTGATGCTACACCAAA 870
 Db 597 CTGCCACCTGATCTCTCTTCCGACATGTGTCTCTGTATGTTGATGCTACACCAAA 656
 Oy 871 ATACAGGAGGTTTCATAGATTTGACACTAATCTCTCTATCCACCTGGTACTGGGA 930
 Db 657 ATACAGGAGGTTTCATAGATTTGACACTAATCTCTCTATCCACCTGGTACTGGGA 716
 Oy 931 AAACCTGCTGAAGATCTGTGTTTCATCTTGCCCTTCAATTAATGCAAGTCTCATATTAC 990
 Db 717 GAACCTGCTGAAGATCTGTGTTTCATCTTGCCCTTCAATTAATGCAAGTCTCATATTAC 776
 Oy 991 CGTGTGATGAGATGATCTTGCCGCTCAAGATGTCCGACATGCTCTCTGCGCCAA 1050
 Db 777 TGTGTGATGAGATGATCTTGCCGCTCAAGATGTCCGACATGCTCTCTGCGCCAA 836
 Oy 1051 AGAAAGACAGAGATCTTTCGAAGATGACACAGATGTGTGTGTGTGTGTGTGTGT 1110
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 Oy 1111 CATGCTGT 1170
 Db 897 TATGCTGT 956
 Oy 1171 AGAACTACGTTCCGACATGTTCTTGGACATCTTGGACATGCTGTAGTTACACAAACG 1230
 Db 957 AGAACTACGTTCCGACATGTTCTTGGACATCTTGGACATGCTGTAGTTACACAAACG 1016
 Oy 1231 CTGCTCAACCCAGTCTTATGATTTCTGTGATGAAACTTCAACGATGCTTGAGGA 1290
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 Oy 1291 GTTGTGTATCCCAACCTTCTTCAACATTTGAGCAACAAATCTCACTCGATTTCTGAGAA 1350
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 Oy 1411 TCTGAGACAGAACTGCTCCGTTGCTTACAGAGGCTCATGCTGCTTCCGACTTTCAC 1470
 Db 1197 TCTGAGAGCAGAACTGCTCCGTTGCTTACAGAGGCTCATGCTGCTTCCGACTTTCAC 1256
 Oy 1471 AAGCTTAAGAGCAGCAATGATGTGAAGAGTGTGCTTCAAGAAATGTGTAGAGAGCTCT 1530
 Db 1257 AAGCTTAAGAGCAGCAATGATGTGAAGAGTGTGCTTCAAGAAATGTGTAGAGAGCTCT 1316
 Oy 1531 AATTTCTAGGAAGTGTGCTTGTAGTCAATCCAACTCTTCTCTGCGCCACTCT 1590
 Db 1317 GGTTCCTGAGAAA---CCATCTGATCTGCTGCAATTCAAAGTCAATCTCTCTGCTGCTTCTC 1373

Oy 1591 GCTTCGACATTTAGAG 1606
 Db 1374 ACTTCGACATGAGAG 1389
 RESULT 12
 US-08-387-707-13
 : Sequence 13, Application US/08387707
 : Patent No. 6265563
 : GENERAL INFORMATION:
 : APPLICANT: EVANS, CHRISTOPHER J.
 : APPLICANT: KEITH, DUANE E.
 : TITLE OF INVENTION: OPIOID RECEPTOR GENES
 : NUMBER OF SEQUENCES: 18
 : CORRESPONDENCE ADDRESS:
 : ADDRESS: MORRISON & FOERSTER
 : STREET: 2000 Pennsylvania Avenue, N.W. Suite 5500
 : CITY: Washington
 : STATE: DC
 : COUNTRY: USA
 : ZIP: 20006-1888
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/387,707
 : FILING DATE: 10-SEP-1995
 : CLASSIFICATION: 536
 : ATTORNEY/AGENT INFORMATION:
 : NAME: MURASHIGE, KATE H.
 : REGISTRATION NUMBER: 29,959
 : REFERENCE/DOCKET NUMBER: 22000-20526, 20
 : TELEPHONE: (202) 887-1500
 : TELEFAX: (202) 887-0763
 : INFORMATION FOR SEQ ID NO: 13:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 830 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: Linear
 : US-08-387-707-13
 Query Match 43.4%; Score 698.4; DB 4; Length 830;
 Best Local Similarity 88.2%; Pred. No. 5.8e-177;
 Matches 721; Conservative 0; Mismatches 94; Indels 2; Gaps 2;
 Oy 527 AGATACACCAAGATGAGAGCTGCCACCAACATCTACATTTTCAACCTTGCTGGCAGT 586
 Db 15 AGATACACCAAGATGAGAGCTGCCACCAACATCTACATTTTCAACCTTGCTGGCAGT 73
 Oy 587 GCCTTAGCCACAGTACCTGCTTCCAGAGTGTGAATTAATGGAACATGGCCA 646
 Db 74 GCCTTAGCCACAGTACCTGCTTCCAGAGTGTGAATTAATGGAACATGGCCA 133
 Oy 647 TTTGGAACCATCTTTGGAAGATAGTATGATTCATAGATTTACTATAACATGTTCCAGC 706
 Db 134 TTTGGAACCATCTTTGGAAGATAGTATGATTCATAGATTTACTATAACATGTTCCAGC 193
 Oy 707 ATATTACCCCTCTGCACATGATGTTGATGATCATTTGCGACCTGTCAG 766
 Db 194 ATATTACCCCTCTGCACATGATGTTGATGATCATTTGCGACCTGTCAG 253
 Oy 767 GCCTTAGATTTCCGAGTCCCGGAAATGCCAAATTAATGCTGCACTGATCTCTC 826
 Db 254 GCCTTAGATTTCCGAGTCCCGGAAATGCCAAATTAATGCTGCACTGATCTCTC 313
 Oy 827 TCTTAGGCAATTTGCTTCTGCTGATATGTTCAATGCTTACACAAATTAAGAGCAAGTTCC 886

APPLICATION NUMBER: US/08/147,592A
FILING DATE: 05-NOV-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/100,694
FILING DATE: 30-JUL-1993
CLASSIFICATION: 435
APPLICATION NUMBER: 08/066,296
FILING DATE: 20-MAY-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: ARCD:105
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
TELEX: N/A
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2272 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 12..1127
US-08-147-592A-3

Query Match 27.5%; Score 443.2; DB 3; Length 2272;
Best Local Similarity 67.3%; Pred. No. 9,7e-109;
Matches 641; Conservative 0; Mismatches 308; Indels 3; Gaps 1;

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DB 142 CGTCCCTGCGCCTTACGATCCGATCCGCGCTCTACTCGCTGCTGCGCAGTGGGCG 201
QY 492 TCTTGGAACTTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 551
DB 202 TTTGGGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 261
QY 552 CCAACATCTACATTTTCAACCTTGGCTGCGAGATGCGCTTACGACCAAGTACCTGCGCT 611
DB 262 CCAACATCTACATTTTCAACCTTGGCTGCGAGATGCGCTTACGACCAAGTACCTGCGCT 321
QY 612 TCCAGAGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 671
DB 322 TCCAGAGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 381
QY 672 TGATCTCATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 731
DB 382 TGATCTCATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 441
QY 732 TTGATCATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 791
DB 442 TGATCTCATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 501
QY 792 ATGCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 851
DB 502 AGGCCAAAGCTATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 561
QY 852 TGTTCATGCTACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 911
DB 562 TGTTCATGCTACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 621
QY 912 ATCCAACTGCTACTGGGAAACCTGCTGAAGATCTGTGTTTCAATCTTGCCTTCATTA 971
DB 622 GTCCAGCTGCTACTGGGAAACCTGCTGAAGATCTGTGTTTCAATCTTGCCTTCATTA 681
QY 972 TGCCAGTCTGCTACTGGGAAACCTGCTGAAGATCTGTGTTTCAATCTTGCCTTCATTA 1031
DB 1031 TGCCAGTCTGCTACTGGGAAACCTGCTGAAGATCTGTGTTTCAATCTTGCCTTCATTA

DB 682 TGCCAGTCTGCTACTGGGAAACCTGCTGAAGATCTGTGTTTCAATCTTGCCTTCATTA 741
QY 1032 GCATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1091
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QY 1092 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1151
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QY 1152 AAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1208
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DB 922 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 981
QY 1269 ACTTCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1328
DB 982 ACTTCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1041
QY 1329 ACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
DB 1042 GTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1093

Search completed: May 1, 2002, 22:15:36
Job time: 4258 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 1, 2002, 18:48:26 ; Search time 1541.38 Seconds

(without alignments)
11224.165 Million cell updates/sec

Title: US-08-305-518-7

Perfect score: 1610
Sequence: 1 CGGATGACCTCTGTGAACCT.....GCTCTGACATTAGAGGCCG 1610

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estfun:*
2: em_esthum:*
3: em_estlin:*
4: em_estom:*
5: em_estpl:*
6: em_estba:*
7: em_estro:*
8: em_estov:*
9: em_htc:*
10: gb_est1:*
11: gb_est2:*
12: gb_htc:*
13: gb_gss:*
14: em_gss_fun:*
15: em_gss_hum:*
16: em_gss_inv:*
17: em_gss_pln:*
18: em_gss_pro:*
19: em_gss_rod:*
20: em_gss_vrt:*
21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	323.6	20.1	520	13	B82759 RPC11-17K2
C 2	322.2	20.0	1053	13	CNS04C2T
C 3	227	14.1	525	13	A0767579 HS_3206.A
C 4	222.2	13.8	389	10	BE649947 UI-M-BH3-
C 5	213.8	13.3	836	13	CNS02261
C 6	211	13.1	877	13	CNS02SC2
C 7	191	11.9	842	13	CNS02SRU
C 8	186.8	11.6	710	13	CNS01ZMG
C 9	184.2	11.4	433	10	AM489031
C 10	158.6	9.9	927	13	CNS04RP2
C 11	158.2	9.8	881	13	CNS03JCN
C 12	155.4	9.7	654	10	AM373832

13	153.8	9.6	702	13	A2966515
14	144.8	9.0	530	11	BF193020
C 15	137.6	8.5	427	10	AM047705 UI-M-BH1-
C 16	136.4	8.5	245	13	AQ488720 RPC1-11-2
17	130.4	8.1	642	10	BE252309 601114162
18	127.4	7.9	741	11	BI224313 602940621
19	125.6	7.8	888	11	BF676176 602084171
20	124	7.7	546	13	A2226406 RPC1-23-8
21	124	7.7	904	11	BG329444 602429002
22	123.8	7.7	937	13	CNS03SGG
23	122	7.6	530	11	BF073470 220178 MA
C 24	117.2	7.3	995	13	CNS04ROE
25	116.2	7.2	832	10	AL536712
26	115.4	7.0	183	11	R81583
27	112.2	7.0	638	10	AM919332
28	108	6.7	656	10	AL119185
29	107.2	6.7	534	10	AM652898
30	105.6	6.6	563	13	A2357931
C 31	98.2	6.1	794	13	CNS01WC1
32	98	6.1	697	11	BG471950
C 33	92.6	5.8	992	13	CNS022ZG
34	90.8	5.6	606	11	BG025021
C 35	90.8	5.6	844	13	CNS03CLX
36	89	5.5	153	11	R31984
37	88.6	5.5	546	11	BG552112
38	88	5.5	213	10	BE388668
C 39	87	5.4	549	11	BE381449
40	87	5.4	954	10	AL556152
41	86.6	5.4	884	11	BG182330
42	84.4	5.2	789	11	BG205056
43	83.2	5.1	781	11	BG681003
44	82	5.1	1045	11	BG404113
C 45	80.4	5.0	901	13	CNS01SK5

ALIGNMENTS

RESULT 1
B82759/C
LOCUS
DEFINITION
B82759 520 bp DNA
RPC11-17K2.TP RPC1-11 Homo sapiens genomic clone RPC1-11-17K22,
DNA sequence.
B82759
B82759.1 GI:2869782
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (Bases 1 to 520)
Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and
Venter,J.C.
Unpublished (1998)
Use of BAC End Sequences for Sequence-Ready Map Building (1998)
JOURNAL
COMMENT
Other GSSs: RPC11-17K2.TVB
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are derived from the human BAC library RPC1-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.bufileo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.bufileo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/cdb/humgen/bac_end_search/bac_end_search.html
Seq primer: SP6
Class: BAC ends.
Location/Qualifiers

FEATURES


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Db 263 CAGAACCTGCTGTGTGGTGGACACCTGTCATCCCGCTGGGCTACATGAACAG 204
QY 1231 CTGGCTCAACCCAGTCCCTTATGATTTCTGGATGAACAACTTCAAGAGATCTTCAGAGA 1290
I 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
Db 203 CAGCTCAACCCGGGTCTTACGCTCTCTGACGACGAGACTTCAAAAGGCTCTTCAGAGA 144
QY 1291 GTTCTGATCCCAACACTCTTCCAACTTGAGCAACAACACTCCACTCGA 1339
I 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
Db 143 CTCTGGCTGGCCCGCGCTCCCGCTCGAGMACAGACGCTTCTCCAGA 95

RESULT 3
A0767579/c 525 bp DNA GSS 28-JUL-1999
LOCUS HS.3206.AL.E05.F7C.C1F Approved Human Genomic Sperm Library D Homo
DEFINITION sapiens genomic clone Plate=3206 Col=9 Row=I, DNA sequence.
ACCESSION A0767579 GI:5645695
VERSION A0767579.1 GI:5645695
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 525)
AUTHORS Mahairas,G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 3206 row: I column: 9
Seq primer: T7
Class: BAC ends
High quality sequence stop: 525.
Location/Qualifiers
1. 525
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=3206 Col=9 Row=I"
/clone_lib="C1F Approved Human Genomic Sperm Library D"
/sex="male"
/note="organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
BASE COUNT 123 a 139 c 126 g 133 t 4 others
ORIGIN
Query Match 14.1% Score 227; DB 13; Length 525;
Best Local Similarity 81.4%; Pred. NO. 9.3e-50;
Matches 263; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 216 GTGGCCCGCCGCGCTGACATGACAGACAGCGCTGCCCGCCAGCAACCCAGCAATT 275
I 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
Db 521 GTGGACGACAGACGCTCAAACTATGACAGACAGCGTCCATGTGACCGCAGTAATAT 462
QY 276 GCACTGATGCTTGGCGTACCAAGTTGCTCCCGACGACCCAGCCGGTTCTGGGTCA 335
I 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
Db 461 GAATGATGCTTACGCTACCAAGTTGCTCCCGACGACCTACCAACCGGTTCTTAGGTCA 402
QY 336 ACTGTGCCACTTATGAGGCAACCTGTCGCGACCATGGGTCCGACCGGACCGACCTGG 395
I 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
Db 401 ACTGTGCCATTATGATGGCAACATGTCTTACCATGTGGGTGACAGACCGCCGCTCTGG 342

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QY 396 GCGGAGACAGACGCTGTGCCCTCCGACCGGACGCTCCCTCATGATCAGCGGCATCAGA 455
I 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
Db 341 GAGGAGACAGACGCTGTGCTTGGCTTGACAGACGAGTCCCTCATGATCAGCGGCATCAGA 282
QY 456 TCATGGCCCTCTACTCCATGCTGTGCTGGGCGCTTTCGGAATCTCTGCTATGT 515
I 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
Db 281 TCATGGCCCTCTACTCCATGCTGTGCTGGGCGCTTTCGGAATCTCTGCTATGT 222
QY 516 ATGTGATTCATGATACCAAG 538
I 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
Db 221 ATGTGATTCATGATACCAAG 199

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RESULT 4
BE649947 389 bp mRNA EST 06-SEP-2000
LOCUS UI-M-BH3-asd-d-09-0-UI.r1 NIH_BMAP_M.S4 Mus musculus cDNA clone
DEFINITION UI-M-BH3-asd-d-09-0-UI 5', mRNA sequence.
ACCESSION BE649947
VERSION BE649947.1 GI:9975771
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 389)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mestr@mail.nih.gov
CDNA Library Preparation: M.B. Soares Lab Clone Distribution:
Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It
should be noted that Bento Soares is generating a small number of
additional specialized non-redundant arrays of BMAP cDNAs whose
availability will be considered under appropriate and limited
collaborative arrangements
Seq primer: M13 Reverse.
Location/Qualifiers
1. 389
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-M-BH3-asd-d-09-0-UI"
/clone_lib="NIH_BMAP_M.S4"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The
NIH_BMAP_M.S4 library is a subtracted library of a series,
ultimately derived from a mixture of individually tagged
normalized libraries from ten regions of the mouse brain
(cerebellum, brain stems, olfactory bulbs, hypothalamus,
cortex, amygdala, basal ganglia, pineal gland, striatum,
hippocampus) after a series of subtractions to reduce the
representation of cDNAs from which ESTs had already been
generated. The following serially subtracted libraries
were generated in this process: NIH_BMAP_M.S4,
NIH_BMAP_M.S3.3, NIH_BMAP_M.S3.2, NIH_BMAP_M.S3.1,
NIH_BMAP_M.S2, NIH_BMAP_M.S1. The subtracted library
(NIH_BMAP_M.S4) was constructed as follows: PCR amplified
cDNA inserts from NIH_BMAP_M.S3.3, NIH_BMAP_M.S3.2, and
NIH_BMAP_M.S3.1 clones from which 3' ESTs had been derived
was used as a driver in a hybridization with a pool of
the NIH_BMAP_M.S3.3, NIH_BMAP_M.S3.2, and NIH_BMAP_M.S3.1
libraries in the form of single-stranded circles. The

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FEATURES

source

remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the NIH-BMAP_M_S4 library. This procedure has been previously described (Bonald, Lennon and Soares, Genome Research 6:791-806, 1996).

BASE COUNT 82 a 120 c 94 g 92 t 1 others
ORIGIN

Query Match 13.8%; Score 222.2; DB 10; Length 389;
Best Local Similarity 73.2%; Pred. No. 1.6e-48;
Matches 284; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

QY 500 AACTTCCTGCTCATGTATGTGTGATACACCAAGATGAAGACGCCACCAATC 559
DB 2 AACGTGCTGCTCATGTATGTGTGATACACCAAGATGAAGACGCCACCAATC 61
QY 560 TACATTTTCAACCTTGTCTGTCAGATGCTTACACCAAGATGAAGACGCCACCAATC 619
DB 62 TACATTTTCAACCTTGTCTGTCAGATGCTTACACCAAGATGAAGACGCCACCAATC 121
QY 620 GTGAATTAACCTTGTCTGTCAGATGCTTACACCAAGATGAAGACGCCACCAATC 679
DB 122 GCCAAGTACCTTGTCTGTCAGATGCTTACACCAAGATGAAGACGCCACCAATC 181
QY 680 ATGATTAACCTTGTCTGTCAGATGCTTACACCAAGATGAAGACGCCACCAATC 739
DB 182 ATGATTAACCTTGTCTGTCAGATGCTTACACCAAGATGAAGACGCCACCAATC 241
QY 740 TACATTTTCAACCTTGTCTGTCAGATGCTTACACCAAGATGAAGACGCCACCAATC 799
DB 242 TACATTTTCAACCTTGTCTGTCAGATGCTTACACCAAGATGAAGACGCCACCAATC 301
QY 800 ATGATTAACCTTGTCTGTCAGATGCTTACACCAAGATGAAGACGCCACCAATC 859
DB 302 CTGATTAACCTTGTCTGTCAGATGCTTACACCAAGATGAAGACGCCACCAATC 361
QY 860 GCTACCAACCAATTAACCTTGTCTGTCAGATGCTTACACCAAGATGAAGACGCCACCAATC 887
DB 362 GCAGTGAACCAATTAACCTTGTCTGTCAGATGCTTACACCAAGATGAAGACGCCACCAATC 389

RESULT 5
CNS02261 836 bp DNA GSS 12-MAY-2000
LOCUS Tetraodon nigroviridis genome survey sequence T7 end of clone
DEFINITION 227103 of library G from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION AL177778
VERSION AL177778.1 GI:7815835
KEYWORDS GSS: genome survey sequence.
SOURCE
ORGANISM Tetraodon nigroviridis.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.

REFERENCE 1 (bases 1 to 836)
AUTHORS Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bounneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 836)
AUTHORS Roest-Crollius, H., Jaillon, O., Dasilva, C., Bounneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brothier, P., Quetier, F., Saurin, W. and Weissenbach, J.
TITLE Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
JOURNAL Unpublished

REFERENCE 3 (bases 1 to 836)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/tetraodon>.

FEATURES
SOURCE
1..836
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="227103"
/contig="G"
/note="Genoscope sequence ID : C0AG227AE02UP1-end : T7"

BASE COUNT 190 a 240 c 203 g 197 t 6 others
ORIGIN

Query Match 13.3%; Score 213.8; DB 13; Length 836;
Best Local Similarity 75.4%; Pred. No. 3.7e-46;
Matches 266; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY 527 AGATTAACCAAGATGAAGATGCTTACCAACATTTTCAACCTTGTCTGTCAGAT 586
DB 269 AGATTAACCAAGATGAAGATGCTTACCAACATTTTCAACCTTGTCTGTCAGAT 328
QY 587 GCTTACCAACCAAGATGAAGATGCTTACCAACATTTTCAACCTTGTCTGTCAGAT 646
DB 329 GCTTACCAACCAAGATGAAGATGCTTACCAACATTTTCAACCTTGTCTGTCAGAT 388
QY 647 TTTGAACCAATTAACCTTGTCTGTCAGATGCTTACCAACATTTTCAACCTTGTCTGTCAGAT 706
DB 389 TTTGAACCAATTAACCTTGTCTGTCAGATGCTTACCAACATTTTCAACCTTGTCTGTCAGAT 448
QY 707 ATATTACCACTTGTCTGTCAGATGCTTACCAACATTTTCAACCTTGTCTGTCAGAT 766
DB 449 ATATTACCACTTGTCTGTCAGATGCTTACCAACATTTTCAACCTTGTCTGTCAGAT 508
QY 767 GCTTACCAACCAAGATGAAGATGCTTACCAACATTTTCAACCTTGTCTGTCAGAT 826
DB 509 GCTTACCAACCAAGATGAAGATGCTTACCAACATTTTCAACCTTGTCTGTCAGAT 568
QY 827 TCTTACCACTTGTCTGTCAGATGCTTACCAACATTTTCAACCTTGTCTGTCAGAT 879
DB 569 TCTTACCACTTGTCTGTCAGATGCTTACCAACATTTTCAACCTTGTCTGTCAGAT 621

RESULT 6
CNS02SC2 877 bp DNA GSS 14-MAY-2000
LOCUS Tetraodon nigroviridis genome survey sequence PUC-Or1 end of clone
DEFINITION 161106 of library G from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION AL211691
VERSION AL211691.1 GI:7870510
KEYWORDS GSS: genome survey sequence.
SOURCE
ORGANISM Tetraodon nigroviridis.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.

REFERENCE 1 (bases 1 to 877)
AUTHORS Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bounneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 877)
AUTHORS Roest-Crollius, H., Jaillon, O., Dasilva, C., Bounneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brothier, P., Quetier, F.,

TITLE	Saurin, W. and Weissbach, J.			
JOURNAL	Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence			
REFERENCE	Unpublished			
AUTHORS	3 (bases 1 to 877)			
TITLE	Genoscope.			
JOURNAL	Direct Submission			
COMMENT	Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases. This sequence is a single read and was generated as part of a large scale clone-end and sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/tetraodon .			
FEATURES	location/Qualifiers			
source	1..877			
	/organism="Tetraodon nigroviridis"			
	/db_xref="taxon:99883"			
	/clone="161H06"			
	/clone_1lb="G"			
	/note="Genoscope sequence ID : C0AG161DD03SP1-end ; PUC-Orig"			
BASE COUNT	201 a	249 c	214 g	197 t
ORIGIN	16 others			

Query Match	13.1%	Score 211	DB 13	Length 877
Best Local Similarity	74.2%	Pred. No. 2	1e 45	
Matches 262	Conservative	3	Mismatches 88	Indels 0
				Gaps 0

QY	527	AGATGACCAGATGAAGTCTGCCACCAACATCTCAATTTCAACCTTGCGAGAT	586
Db	348	AGGTACACCAAGATGAAGACCGCCACMAACATCTACATCTTCAACCTGCTTGCGCCAC	407
QY	587	GCCTTAGCCACAGTATACCCTGCCCTTCCAGAGTGTGAATTAACCTAATGGGAACATGGCCA	646
Db	408	GCTTAGGCCACACGAGCACCTCCCTCCCTCCACAGACGGCCAAAGTACCTGATGAACACGTGGTGG	467
QY	647	TTTGGAAACCATCCTTTGGCAAGATAGTATCTCATAGATTACTATATACATGTTCAACACAC	706
Db	468	TTCCGGGAGAGTGTCTGTGCAAACTGGTTCATCGCATTTGACTACATACAACTGTTTCAACACAC	527
QY	707	ATATTACACCTCTGCACCATAGTGTTCATGATACATTGCAGTCCACCCCTGTCAAG	766
Db	528	ATCTTCACAGCTACCATATATGAGCGTCGACCGCCACAGTTGCCGTTGGCCACCCGGGTCGG	587
QY	767	GCCTTAGATTTCCGTACTCTCCCGAATATGCCAAATTTATCAATGTCTGCACATGCAATCCG	826
Db	588	GGCGGAGCACTCCGCACACCCGCCAAGGCCAAATATCATCACTAACGTGTTCATCTGTGATCCG	647
QY	827	TCTTTCAGCCATTGGTCTTCTCTGTAAATGTTTCATAGCTACACAAATATACAGGCA	879
Db	648	TCTCATGCCGCTGTGAGTACCGGTGTGTATGATGACAGCSACCAAGAGAGMGA	700

RESULT	7
CNS02SKU/c	
LOCUS	
DEFINITION	CNS02SKU 842 bp DNA GSS 15-MAY-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 162E18 of library G from Tetraodon nigroviridis, genomic survey sequence.
ACCESSION	AL212007
VERSION	AL212007.1 GI:7870826
KEYWORDS	GSS: genome survey sequence.
SOURCE	Tetraodon nigroviridis.
ORGANISM	Tetraodon nigroviridis
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.
REFERENCE	1 (bases 1 to 842)
AUTHORS	Roeest-Crollius,H., Jallou,O., Dasilva,C., Fizames,C., Fisher,C., Bonneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.
TITLE	Characterization and repeat analysis of the compact genome of the

JOURNAL REFERENCE AUTHORS	TITLE
JOURNAL REFERENCE AUTHORS	freshwater pufferfish Tetraodon nigroviridis
TITLE	Unpublished
JOURNAL REFERENCE AUTHORS	2 (bases 1 to 842)
TITLE	Bernot-Crolius,H., Jallon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brothier,P., Queller,F., Saurin,W. and Weissbach,J.
JOURNAL REFERENCE AUTHORS	Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
TITLE	Unpublished
JOURNAL REFERENCE AUTHORS	3 (bases 1 to 842)
TITLE	Genoscope. Direct Submission
JOURNAL COMMENT	Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon .
FEATURES	Location/Qualifiers
SOURCE	1..842
	/organism="Tetraodon nigroviridis"
	/db_xref="taxon:99883"
	/clone="162E18"
	/clone_lib="G"
	/note="Genoscope sequence ID : COAG162BC09LP1-end : 77"
BASE COUNT	135 a 272 c 285 g 141 t 9 others
ORIGIN	

Query Match	11.9%	Score 191;	DB 13;	Length 842;
Best Local Similarity	62.28%	Pred. No. 4.5e-40;		
Matches 306; Conservative	6;	Mismatches 177;	Indels 3;	Gaps 1;

QY	888	TAGATTTGACACTAAACATTTCTCTCTATCCAACTGGTACTGTGGAAAAACCTGGCGAAGACT	947
Db	781	TGGTGTGGCGCGCTGCAGTTCCTCCGGAGCGCGGGCTGGTACTGGAGACACGCTCTCAAGATCT	722
QY	948	GATTTTTCATCTTGGCCCTTTCATTTATGCCAGTCTCATCTTACCGCTGTGTATGGACTGA	1007
Db	721	GCGTCTTCGTTTGGCCCTTCGTCGTGGTTCGCCGCTGTGTCATCAGCGCTCTGCAAGCGCTTGA	662
QY	1008	TGATTTTCGCGCTCAAGAGTGTCCGCATGTCCTCTGGCTGCCAAAAGAAAGACAGAAATC	1067
Db	661	TGATCTCTGCGCTCAGAGAGCGTGGCCCGCGCTCTCGCGGCCCAAGAGAAAGGACSGCAACA	602
QY	1068	TTTGAAGGATACCAAGAGTGGTGTCTGTGTGTGTGGTGTGTGTATCTCTCTGTCTGGACTC	1127
Db	601	GAGCGCGCATCACCGCATCGGCTGTGGGCTGTGTGTGTGTGGCGCGCKTCTGTGCTGTGGAGCGC	542
QY	1128	CCATTCACATTTAGCTGTCTCATFTTAAAGCCTGTGTACAAATCCAGAA--CTTAGCTTCC	1184
Db	541	CCATCCACATCTCTCATCTACAGGGGGAAGAGCGCGGTGTGAGAACGACGCGCAGGCACTCGTGG	482
QY	1185	AGACTGTTTCTTGGCACTTTCGATTTGCTCTAGGTTTACACAACACAGCTCCTCAACCCAG	1244
Db	481	TGGTGGCGCGGCTGGGCACTGGGCAATCGGCTGTGGGCAACACACAGCAGCTCAACCCGCG	422
QY	1245	TCTTTTATGCACTTCTGSGATGAAAACTTCAACGATGCTTACAGAGAGTTCGTATCCAA	1304
Db	421	TCTCTNACGCCCTCTCTGTGAGCAGAACTKTCAGAAGGCGCTTCCGGATTCATGTGCTCCCT	362
QY	1305	CCTCTTCCACATTTGAGCAACAAAACCTCACCTGATTTCTGACAACTATAGACACAC	1364
Db	361	GCCGAGCGCGGAGCGGCGGCGGACCGCCCTGTGGCCGAGCGCGCACCCCGCCAGAGGAGCCG	302
QY	1365	CCTCCACGGCCA	1376
Db	301	CCTCTGCTCKGCA	290

RESULT	8
CNS01ZMG	
LOCUS	CNS01ZMG
DEFINITION	Tetradon nigroviridis genome survey sequence pUC-ori end of clone
	710 bp DNA GSS 12-MAY-2000

[illegible]

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RESULT      9
LOCUS       AM489031/c
DEFINITION  AM489031 433 bp mRNA EST 24-FEB-2000
            UI-M-BH3-ascl-d-09-0-UI.s1 NIH_BMAP_M_S4 Mus musculus cDNA clone
            UI-M-BH3-ascl-d-09-0-UI 3', mRNA sequence.
ACCESSION   AM489031
VERSION     AM489031.1 GI:7059301
KEYWORDS    EST.
SOURCE      house mouse.
ORGANISM    Mus musculus
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE       1 (bases 1 to 433)
            Bonaldo,M.F., Lennon,G. and Soares,M.B.
            Normalization and subtraction: two approaches to facilitate gene
            discovery
JOURNAL     Genome Res. 6 (9), 791-806 (1996)
MEDLINE     97044477
COMMENT     Contact: Chih, H
            National Institute of Mental Health
            6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
            20892-9643, USA
            Tel: 301 443 31706
            Fax: 301 443 9890
            Email: mesf@mail.nih.gov
            Oligo-dT track not found, Not 1 site shown in beginning of sequence
            is likely internal to the message. cDNA library preparation: M.B.
            Soares Lab Clone distribution: Researchers may obtain BMAP cDNA
            clones from RESEARCH GENERICS. It should be noted that Bento Soares
            is generating a small number of additional specialized
            non-redundant arrays of BMAP cDNAs whose availability will be
            considered under appropriate and limited collaborative arrangements
            Seq primer: M13 Forward
            POLYA-NO.
FEATURES
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                /dev_stage="27-32 days"
                /lab_host="DH10B (Life Technologies)"
                /note="Vector: pT73D-Pac (Pharmacia) with a modified
                polylinker. Site.1: Not I; Site.2: Eco RI; The
                NIH_BMAP_M_S4 library is a subtracted library of a series,
                ultimately derived from a mixture of individually tagged
                normalized libraries from ten regions of the mouse brain
                (cerebellum, brain stems, olfactory bulbs, hypothalamus,
                cortex, amygdala, basal ganglia, pineal gland, striatum,
                hippocampus) after a series of subtractions to reduce the
                representation of cDNAs from which ESTs had already been
                generated. The following serially subtracted libraries
                were generated in this process: NIH_BMAP_M_S2,
                NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, NIH_BMAP_M_S3.1,
                NIH_BMAP_M_S2, NIH_BMAP_M_S1. The subtracted library
                (NIH_BMAP_M_S4) was constructed as follows: PCR amplified
                cDNA inserts from NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and
                NIH_BMAP_M_S3.1 clones from which 3' ESTs had been derived
                was used as a driver in a hybridization with a pool of
                the NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.1
                libraries in the form of single-stranded circles. The
                remaining single-stranded circles (subtracted library)
                was purified by hydroxyapatite column chromatography,
                converted to double-stranded circles and electroporated
                into DH10B bacteria (Life Technologies) to generate the
                NIH_BMAP_M_S4 library. This procedure has been previously
                described (Bonaldo, Lennon and Soares, Genome Research
                6:791-806, 1996)
                TAG_LIB=NIH_BMAP_M_S4
                TAG_TISSUE=cerebellum
                TAG_SEQ=CGNA"

```


This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at

TITLE	Direct Submission
JOURNAL	Submitted (12-APR-2000) to the EMBL/Genbank/DBJ databasess
COMMENT	This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetradon nigroviridis

MEDLINE 97044477
Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mestr@mail.nih.gov

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag served to identify it as a clone from the normalized cerebellum library cDNA library Preparation: M.B. Soares Lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined.
Seq primer: M13 Forward
POLYA-Yes.

FEATURES
Source Location/Qualifiers

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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="01-M-BH1-alo-f-04-0-01"
/clone_1id="NIH_BMAP_M_S2"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/note="vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The NIH_BMAP_M_S2 library is a subtracted library derived from NIH_BMAP_M_S1, which in turn is a subtracted library derived from a mixture of normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hippocampus). The driver used for subtraction consisted of a pool of 5,000 clones from the NIH_BMAP_M_S1 library and a pool of 2,000 clones obtained from non-normalized and normalized mouse brain spinal cord libraries.
TAG_LIB="NIH_BMAP_M_S2"
TAG_TISSUE="cerebellum"
TAG_SEQ="GACTC"

BASE COUNT 119 a 104 c 107 g 97 t
ORIGIN

Query Match 8.5%; Score 137.6; DB 10; Length 427;
Best Local Similarity 59.9%; Pred. No. 6.1e-26;
Matches 230; Conservative 0; Mismatches 154; Indels 0; Gaps 0;

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DB 353 CTACACATGTTTACACAGCATATTCACCTGACCATGAGTGTGAGACCGTTATGTAGC 294
QY 748 AGTCTGCCACCCCTGCAAGCCCTTAGATTCCTGACTCCCGAAATGCCAAATATCA 807
DB 293 TATCTGCCACCCCTTATCGCTTGTGATGTTGACATCCAGTAAAGCCAGCCGTAA 234
QY 808 TGTCTGCACTGATCCCTGCTTCATGATGATGATGATGATGATGATGATGATGATGAT 867
DB 233 TGTGCGCATATGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 174
QY 868 AAATACAGGAGGATTCATAGATTTGATACATTAATTCATTCACCACTGTACTG 927
DB 173 ACAAGTGAAGATGAAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 114
QY 928 GGAAGACCTGCTGAAGATGCTGTTTCATCTGCTTCAATATGCCAGTGTCAATCAT 987

DB 113 GGGCCCTGATTTGCAATCCATGCAATCTTCTTCTTCATCATCCCGTTGATCAT 54
QY 988 TACGTTGCTATGACTGATGAT 1011
DB 53 CTGTCTGCTTACAGCCTCATGAT 30

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